

Reptile

Score	E
(bits)	Value

<a href="#">gi 22416427 gb AAM96215.1 </a>	potassium-chloride transporter-3...	<a href="#">1226</a>	0.0
<a href="#">gi 6693798 gb AAF24986.1 </a>	K-Cl cotransporter KCC3 [Homo sap...	<a href="#">1226</a>	0.0
<a href="#">gi 33329252 gb AAQ10026.1 </a>	K-Cl cotransporter KCC3a-X2M iso...	<a href="#">1208</a>	0.0
<a href="#">gi 41281645 ref NP_598410.1 </a>	solute carrier family 12, memb...	<a href="#">1197</a>	0.0
<a href="#">gi 47124056 gb AAH70107.1 </a>	SLC12A6 protein [Homo sapiens]	<a href="#">1184</a>	0.0
<a href="#">gi 33329256 gb AAQ10028.1 </a>	K-Cl cotransporter KCC3a-S2 isof...	<a href="#">1183</a>	0.0
<a href="#">gi 38565928 gb AAH62099.1 </a>	Unknown (protein for MGC:69652) ...	<a href="#">1157</a>	0.0
<a href="#">gi 22416428 gb AAM96216.1 </a>	potassium-chloride transporter-3...	<a href="#">1154</a>	0.0
<a href="#">gi 19526769 ref NP_598409.1 </a>	solute carrier family 12, memb...	<a href="#">1134</a>	0.0
<a href="#">gi 34856648 ref XP_342490.1 </a>	similar to K-Cl cotransporter ...	<a href="#">1117</a>	0.0
<a href="#">gi 7512561 pir  T17275</a>	hypothetical protein DKFZp434D2135.1...	<a href="#">1116</a>	0.0
<a href="#">gi 19110891 gb AAL85335.1 </a>	K-Cl cotransporter KCC3 variant ...	<a href="#">1115</a>	0.0
<a href="#">gi 9507107 ref NP_062102.1 </a>	solute carrier family 12, membe...	<a href="#">865</a>	0.0
<a href="#">gi 45219767 gb AAH66872.1 </a>	Solute carrier family 12, member...	<a href="#">862</a>	0.0
<a href="#">gi 27151684 sp Q28677 S124</a>	<a href="#">RAB1T</a> Solute carrier family 12 m...	<a href="#">862</a>	0.0
<a href="#">gi 6677993 ref NP_033221.1 </a>	solute carrier family 12, membe...	<a href="#">862</a>	0.0

gi 4827006 ref NP_005063.1	solute carrier family 12 (potas...	862	0.0	G
gi 47213488 emb CAF91145.1	unnamed protein product [Tetrao...	859	0.0	
gi 31324218 gb AAP47188.1	potassium-chloride cotransporter...	856	0.0	G
gi 47522728 ref NP_999114.1	K-Cl cotransporter [Sus scrofa...	856	0.0	G
gi 3015641 gb AAC39685.1	erythroid K:Cl cotransporter spli...	837	0.0	G
gi 11968148 ref NP_065759.1	solute carrier family 12 membe...	783	0.0	G
gi 19705463 ref NP_599190.1	solute carrier family 12 membe...	783	0.0	G
gi 12003227 gb AAG43493.1	electroneutral potassium-chlorid...	783	0.0	G
gi 14193696 gb AAK56093.1	K-Cl cotransporter [Mus musculus...	780	0.0	G
gi 28972652 dbj BAC65742.1	mKIAA1176 protein [Mus musculus]	780	0.0	G
gi 3015639 gb AAC39684.1	erythroid K:Cl cotransporter spli...	780	0.0	G
gi 33859680 ref NP_065066.1	solute carrier family 12, memb...	778	0.0	G
gi 6755534 ref NP_035520.1	solute carrier family 12, membe...	773	0.0	G
gi 47847414 dbj BAD21379.1	mFLJ00098 protein [Mus musculus]	773	0.0	G
gi 6330233 dbj BAA86490.1	KIAA1176 protein [Homo sapiens]	772	0.0	G
gi 5730043 ref NP_006589.1	solute carrier family 12 (potas...	767	0.0	G
gi 50753670 ref XP_414082.1	PREDICTED: similar to K-Cl cot...	766	0.0	G
gi 50733496 ref XP_418891.1	PREDICTED: similar to mFLJ0009...	761	0.0	G
gi 32490535 gb AAP84988.1	potassium-chloride cotransporter...	753	0.0	
gi 47225214 emb CAF98841.1	unnamed protein product [Tetrao...	753	0.0	
gi 9651224 gb AAF91094.1	K-Cl cotransporter KCC1 [Mus musc...	707	0.0	G
gi 47223173 emb CAG11308.1	unnamed protein product [Tetrao...	688	0.0	
gi 47220725 emb CAG11794.1	unnamed protein product [Tetrao...	687	0.0	
gi 47213000 emb CAF95392.1	unnamed protein product [Tetrao...	672	0.0	
gi 24762439 ref NP_726378.1	CG5594-PA [Drosophila melanoga...	598	e-169	G
gi 21429886 gb AAM50621.1	GH09271p [Drosophila melanogaste...	597	e-169	G
gi 46409210 gb AAS93762.1	LD02554p [Drosophila melanogaste...	595	e-168	G
gi 22026947 ref NP_571976.2	CG5594-PC [Drosophila melanoga...	594	e-168	G
gi 10440500 dbj BAB15783.1	FLJ00098 protein [Homo sapiens]	531	e-149	G
gi 48096020 ref XP_394587.1	similar to CG5594-PC [Apis mel...	531	e-149	G
gi 10440514 dbj BAB15787.1	FLJ00105 protein [Homo sapiens]	501	e-140	G
gi 34853395 ref XP_217744.2	similar to putative potassium-...	452	e-125	G
gi 25149428 ref NP_500910.2	solute carrier family 12 membe...	440	e-121	G
gi 39584234 emb CAE61609.1	Hypothetical protein CBG05529 [...	438	e-121	
gi 31226974 ref XP_317803.1	ENSANGP00000014479 [Anopheles ...	420	e-115	G
gi 17541928 ref NP_501141.1	solute carrier family 12 membe...	360	2e-97	G
gi 39593544 emb CAE61836.1	Hypothetical protein CBG05808 [...	353	2e-95	
gi 26343083 dbj BAC35198.1	unnamed protein product [Mus mu...	332	3e-89	
gi 18073139 emb CAC80545.1	putative Na-K-Cl cotransporter ...	322	4e-86	
gi 39596034 emb CAE67537.1	Hypothetical protein CBG13060 [...	320	1e-85	
gi 31226957 ref XP_317800.1	ENSANGP00000004794 [Anopheles ...	311	8e-83	G
gi 13507237 gb AAK28520.1	K-Cl cotransporter [Xenopus laevis]	309	3e-82	
gi 17534831 ref NP_495555.1	Na-K-Cl cotransporter (2H716) ...	299	3e-79	G
gi 32484273 gb AAH54325.1	LOC398663 protein [Xenopus laevis]	224	8e-57	G
gi 31226979 ref XP_317804.1	ENSANGP00000024771 [Anopheles ...	208	8e-52	G
gi 50944163 ref XP_481609.1	putative Na+/K+/Cl-cotransport...	206	4e-51	
gi 15208177 dbj BAB63113.1	hypothetical protein [Macaca fa...	202	4e-50	
gi 2582381 gb AAC49874.1	cation-chloride co-transporter [N...	201	1e-49	
gi 9651629 gb AAF91220.1	potassium-chloride cotransporter ...	200	2e-49	

gi 47193414 emb CAG14039.1	unnamed protein product [Tetrao...	194	2e-47	
gi 30691724 ref NP_849732.1	cation-chloride cotransporter,...	194	2e-47	G
gi 6634764 gb AAF19744.1	Strong similarity to gb AF021220 ...	192	4e-47	
gi 47203569 emb CAG13773.1	unnamed protein product [Tetrao...	187	1e-45	
gi 3582769 gb AAC35282.1	erythrocyte K-Cl cotransporter [H...	183	3e-44	G
gi 9651216 gb AAF91090.1	K-Cl cotransporter [Mus musculus]	165	6e-39	G
gi 3925714 emb CAA09464.1	KCC2 protein [Mus musculus]	153	3e-35	G
gi 14043556 gb AAH07760.1	SLC12A7 protein [Homo sapiens]	149	6e-34	G
gi 35505532 gb AAH57624.1	Slc12a5 protein [Mus musculus]	147	2e-33	G
gi 31226967 ref XP_317802.1	ENSANGP00000015001 [Anopheles ...	141	9e-32	G
gi 7512576 pir  T17231	hypothetical protein DKFZp434F076.1 ...	136	4e-30	G
gi 20151457 gb AAM11088.1	GH27027p [Drosophila melanogaste...	133	3e-29	G
gi 52075682 dbj BAD44902.1	putative potassium-chloride cot...	130	2e-28	
gi 38073246 gb AAR10807.1	K-Cl cotransporter KCC3a isoform...	130	3e-28	
gi 50778569 ref XP_427392.1	PREDICTED: similar to solute c...	127	2e-27	G
gi 48119195 ref XP_393214.1	similar to bumetanide sensitiv...	123	3e-26	G
gi 34905658 ref NP_914176.1	putative cation-chloride co-tr...	121	1e-25	G
gi 1673531 gb AAB18960.1	furosemide-sensitive K-Cl cotrans...	120	2e-25	
gi 38073248 gb AAR10808.1	brain-specific K-Cl cotransporte...	111	1e-22	
gi 31236589 ref XP_319440.1	ENSANGP00000014326 [Anopheles ...	111	1e-22	G
gi 13937397 ref NP_113583.1	solute carrier family 12 (pota...	106	4e-21	G
gi 51859114 gb AAH81728.1	Cation-chloride cotransporter 6 ...	105	9e-21	G
gi 13516498 dbj BAB40456.1	cation chloride cotransporter 6...	105	9e-21	G
gi 51094566 gb EAL23818.1	solute carrier family 12 (potass...	104	2e-20	G
gi 9502260 gb AAF88060.1	cation-chloride cotransporter-int...	103	2e-20	G
gi 6179898 gb AAF05702.1	Na+/K+/2Cl- cotransporter [Callin...	101	1e-19	
gi 14486416 gb AAK62044.1	Na+/K+/2Cl- cotransporter [Carci...	101	1e-19	
gi 48101446 ref XP_395129.1	similar to ENSANGP00000014326 ...	100	2e-19	G
gi 13383504 gb AAK21009.1	cation-chloride cotransporter-in...	100	2e-19	
gi 50423949 ref XP_460559.1	unnamed protein product [Debar...	100	3e-19	G
gi 31242251 ref XP_321556.1	ENSANGP00000011560 [Anopheles ...	100	4e-19	G
gi 19705533 ref NP_599232.1	cation-chloride cotransporter ...	99	5e-19	G
gi 25304083 gb AAH40138.1	Unknown (protein for MGC:48843) ...	98	1e-18	
gi 516001 gb AAC48592.1	bumetanide-sensitive Na-K-Cl cotra...	97	2e-18	
gi 1709296 sp P55015 S121	RABIT Solute carrier family 12 me...	97	3e-18	
gi 9507103 ref NP_062007.1	solute carrier family 12, membe...	97	3e-18	G
gi 4557849 ref NP_000329.1	sodium potassium chloride cotra...	97	3e-18	G
gi 1079521 gb AAC52633.1	kidney-specific Na-K-Cl cotranspo...	97	3e-18	G
gi 2290526 gb AAB65150.1	Na-(K)-Cl cotransporter isoform m...	97	3e-18	G
gi 6755532 ref NP_035519.1	solute carrier family 12, membe...	96	7e-18	G
gi 34365781 ref NP_899197.1	solute carrier family 12, memb...	96	7e-18	G
gi 16877251 gb AAH16888.1	Solute carrier family 12, member...	96	7e-18	G
gi 27151793 sp P55014 S121	MOUSE Solute carrier family 12 m...	96	7e-18	G
gi 40950187 gb AAR97733.1	Na-K-Cl cotransporter [Oreochrom...	96	7e-18	
gi 17543066 ref NP_502704.1	solute carrier family 12 membe...	95	1e-17	G
gi 47230656 emb CAF99849.1	unnamed protein product [Tetrao...	95	1e-17	
gi 21483278 gb AAM52614.1	GH09711p [Drosophila melanogaste...	95	1e-17	G
gi 20177071 gb AAM12297.1	RH37201p [Drosophila melanogaster]	95	1e-17	
gi 24644255 ref NP_730939.1	CG31547-PA [Drosophila melanog...	95	1e-17	G

<a href="#">gi 39586961 emb CAE62896.1 </a>	Hypothetical protein CBG07084 [...]	<a href="#">94</a>	3e-17	
<a href="#">gi 2136942 pir  I46497</a>	bumetanide-sensitive Na-K-Cl cotrans...	<a href="#">93</a>	5e-17	
<a href="#">gi 27652641 emb CAD31111.1 </a>	putative sodium-potassium-chlor...	<a href="#">93</a>	5e-17	
<a href="#">gi 2137580 pir  I49269</a>	Na+/K+/Cl-cotransport protein renal ...	<a href="#">93</a>	5e-17	<b>G</b>
<a href="#">gi 47224809 emb CAG06379.1 </a>	unnamed protein product [Tetrao...	<a href="#">92</a>	1e-16	
<a href="#">gi 50752967 ref XP_413814.1 </a>	PREDICTED: similar to bumetani...	<a href="#">91</a>	1e-16	<b>G</b>
<a href="#">gi 15010508 gb AAK77302.1 </a>	GH08340p [Drosophila melanogaste...	<a href="#">91</a>	2e-16	<b>G</b>
<a href="#">gi 31197669 ref XP_307782.1 </a>	ENSANGP00000012928 [Anopheles ...]	<a href="#">91</a>	2e-16	<b>G</b>
<a href="#">gi 23955920 gb AAN40689.1 </a>	putative sodium-potassium-2-chlo...	<a href="#">91</a>	2e-16	
<a href="#">gi 47227672 emb CAG09669.1 </a>	unnamed protein product [Tetrao...	<a href="#">91</a>	2e-16	
<a href="#">gi 40950185 gb AAR97732.1 </a>	Na-K-Cl cotransporter [Oreochrom...	<a href="#">91</a>	2e-16	
<a href="#">gi 47210716 emb CAF92943.1 </a>	unnamed protein product [Tetrao...	<a href="#">90</a>	4e-16	
<a href="#">gi 27652643 emb CAD31112.1 </a>	putative sodium-potassium-chlor...	<a href="#">89</a>	5e-16	
<a href="#">gi 40950183 gb AAR97731.1 </a>	Na-K-Cl cotransporter [Oreochrom...	<a href="#">89</a>	5e-16	
<a href="#">gi 21686589 gb AAM74968.1 </a>	renal Na-K-Cl cotransporter isof...	<a href="#">89</a>	7e-16	
<a href="#">gi 21686587 gb AAM74967.1 </a>	renal Na-K-Cl cotransporter isof...	<a href="#">89</a>	7e-16	
<a href="#">gi 47213642 emb CAF90346.1 </a>	unnamed protein product [Tetrao...	<a href="#">89</a>	9e-16	
<a href="#">gi 596076 gb AAA75600.1 </a>	bumetanide sensitive NaK2Cl cotran...	<a href="#">88</a>	1e-15	
<a href="#">gi 17535967 ref NP_493773.1 </a>	cation-chloride cotransporter-...	<a href="#">88</a>	2e-15	<b>G</b>
<a href="#">gi 50727039 gb AAT81190.1 </a>	Hypothetical protein T04B8.5b [C...	<a href="#">88</a>	2e-15	
<a href="#">gi 50344814 ref NP_001002080.1 </a>	zgc:85961 [Danio rerio] >gi...	<a href="#">88</a>	2e-15	<b>G</b>
<a href="#">gi 4506977 ref NP_000330.1 </a>	solute carrier family 12 (sodiu...	<a href="#">87</a>	3e-15	<b>G</b>
<a href="#">gi 1717801 sp P55017 S123 HUMAN</a>	Solute carrier family 12 me...	<a href="#">87</a>	3e-15	<b>G</b>
<a href="#">gi 7513175 pir  G01202</a>	NaCl electroneutral Thiazide-sensiti...	<a href="#">87</a>	3e-15	<b>G</b>
<a href="#">gi 5759119 gb AAD50984.1 </a>	Na-K-2Cl- cotransporter [Oryctola...	<a href="#">87</a>	3e-15	
<a href="#">gi 1083802 pir  B54145</a>	sodium-chloride transporter, Thiazid...	<a href="#">86</a>	4e-15	
<a href="#">gi 33563368 ref NP_062218.2 </a>	solute carrier family 12, memb...	<a href="#">86</a>	4e-15	<b>G</b>
<a href="#">gi 21686585 gb AAM74966.1 </a>	renal Na-K-Cl cotransporter isof...	<a href="#">86</a>	6e-15	
<a href="#">gi 21686583 gb AAM74965.1 </a>	renal Na-K-Cl cotransporter isof...	<a href="#">86</a>	6e-15	
<a href="#">gi 2599070 gb AAC33139.1 </a>	thiazide-sensitive sodium chlorid...	<a href="#">86</a>	6e-15	
<a href="#">gi 2136267 pir  PC4180</a>	thiazide-sensitive sodium-chloride c...	<a href="#">86</a>	8e-15	
<a href="#">gi 38073244 gb AAR10806.1 </a>	K-Cl cotransporter KCC3b isoform...	<a href="#">85</a>	1e-14	
<a href="#">gi 14547897 ref NP_062288.1 </a>	solute carrier family 12, memb...	<a href="#">85</a>	1e-14	<b>G</b>
<a href="#">gi 24047306 gb AAH38612.1 </a>	Solute carrier family 12, member...	<a href="#">85</a>	1e-14	<b>G</b>
<a href="#">gi 30721813 gb AAP33906.1 </a>	bumetanide-sensitive Na-K-Cl cot...	<a href="#">84</a>	2e-14	<b>G</b>
<a href="#">gi 6677991 ref NP_033220.1 </a>	solute carrier family 12, membe...	<a href="#">84</a>	2e-14	<b>G</b>
<a href="#">gi 2147143 pir  I51307</a>	basolateral Na(+)-K(+)-Cl- cotranspo...	<a href="#">84</a>	2e-14	
<a href="#">gi 1709294 sp P55013 S122 SQUAC</a>	Solute carrier family 12 me...	<a href="#">84</a>	3e-14	
<a href="#">gi 34879509 ref XP_346514.1 </a>	hypothetical protein XP_346513...	<a href="#">84</a>	3e-14	<b>G</b>
<a href="#">gi 27807511 ref NP_777207.1 </a>	solute carrier family 12 (sodi...	<a href="#">84</a>	3e-14	<b>G</b>
<a href="#">gi 13929130 ref NP_113986.1 </a>	solute carrier family 12, memb...	<a href="#">84</a>	3e-14	<b>G</b>
<a href="#">gi 50761390 ref XP_424716.1 </a>	PREDICTED: similar to Solute c...	<a href="#">84</a>	3e-14	<b>G</b>
<a href="#">gi 5081312 gb AAD39342.1 </a>	bumetanide-sensitive Na-K-2Cl cot...	<a href="#">84</a>	3e-14	<b>G</b>
<a href="#">gi 47222533 emb CAG02898.1 </a>	unnamed protein product [Tetrao...	<a href="#">83</a>	4e-14	
<a href="#">gi 50753599 ref XP_414059.1 </a>	PREDICTED: similar to solute c...	<a href="#">83</a>	5e-14	<b>G</b>
<a href="#">gi 48102011 ref XP_392732.1 </a>	similar to CG4357-PA [Apis mel...	<a href="#">81</a>	1e-13	<b>G</b>
<a href="#">gi 290856 gb AAA49272.1 </a>	thiazide sensitine NaCl cotranspor...	<a href="#">80</a>	2e-13	
<a href="#">gi 1581614 prf  2117156A</a>	basolateral Na/K/Cl cotransporter	<a href="#">80</a>	2e-13	
<a href="#">gi 4584410 emb CAB40708.1 </a>	basolateral NaK(2Cl) cotransport...	<a href="#">78</a>	2e-12	
<a href="#">gi 46441770 gb EAL01065.1 </a>	hypothetical protein CaO19.6833 ...	<a href="#">76</a>	5e-12	
<a href="#">gi 34857570 ref XP_345417.1 </a>	similar to K-Cl cotransporter ...	<a href="#">75</a>	8e-12	<b>G</b>
<a href="#">gi 21686581 gb AAM74964.1 </a>	renal Na-K-Cl cotransporter isof...	<a href="#">75</a>	8e-12	
<a href="#">gi 21686579 gb AAM74963.1 </a>	renal Na-K-Cl cotransporter isof...	<a href="#">75</a>	8e-12	

gi 46100179 gb EAK85412.1	hypothetical protein UM04602.1 [...	74	2e-11	
gi 47226271 emb CAG09239.1	unnamed protein product [Tetrao...	72	1e-10	
gi 37575103 gb AAQ93478.1	furosemide-sensitive KCl cotrans...	71	2e-10	
gi 46446456 ref YP_007821.1	putative bumetanide-sensitive ...	70	3e-10	G
gi 44984445 gb AAS53347.1	AFL025Cp [Eremothecium gossypii]...	70	3e-10	G
gi 50292197 ref XP_448531.1	unnamed protein product [Candi...	70	3e-10	G
gi 6319712 ref NP_009794.1	Hypothetical ORF; Ybr235wp [Sac...	70	4e-10	G
gi 50545908 ref XP_500492.1	hypothetical protein [Yarrowia...	69	6e-10	G
gi 50311073 ref XP_455560.1	unnamed protein product [Kluyv...	69	6e-10	G
gi 19112532 ref NP_595740.1	putative membrane transporter ...	69	7e-10	G
gi 45527020 ref ZP_00178221.1	COG0531: Amino acid transpor...	67	2e-09	
gi 17533079 ref NP_495469.1	cation-chloride cotransporter ...	67	4e-09	G
gi 48893479 ref ZP_00326715.1	COG0531: Amino acid transpor...	65	8e-09	
gi 32404944 ref XP_323085.1	hypothetical protein ( AL5134...	65	1e-08	G
gi 47013799 gb AAT08445.1	Na-K-Cl cotransporter isoform 2 ...	64	2e-08	
gi 38073242 gb AAR10805.1	K-Cl cotransporter KCC4 [Rattus ...	64	2e-08	G
gi 24899633 ref NP_705889.1	cation-chloride cotransporter ...	64	2e-08	G
gi 23495278 dbj BAC20265.1	cation-chloride cotransporter 9...	64	2e-08	G
gi 19527414 ref NP_599012.1	solute carrier family 12, memb...	64	3e-08	G
gi 39582293 emb CAE67542.1	Hypothetical protein CBG13067 [...	64	3e-08	
gi 21411274 gb AAH30926.1	Slc12a8 protein [Mus musculus]	63	4e-08	G
gi 20892349 ref XP_147174.1	cation-chloride cotransporter ...	63	4e-08	
gi 10440502 dbj BAB15784.1	FLJ00100 protein [Homo sapiens]	63	4e-08	G
gi 10440351 dbj BAB15711.1	FLJ00010 protein [Homo sapiens]	63	4e-08	G
gi 42551588 gb EAA74431.1	hypothetical protein FG05147.1 [...	62	7e-08	G
gi 48140542 ref XP_397130.1	similar to CG12773-PA [Apis me...	62	1e-07	G
gi 20093291 ref NP_619366.1	Na-K-Cl cotransporter [Methano...	61	2e-07	G
gi 47013797 gb AAT08444.1	Na-K-Cl cotransporter isoform 1 ...	61	2e-07	
gi 45523845 ref ZP_00175172.1	COG0531: Amino acid transpor...	61	2e-07	
gi 39581643 emb CAE71764.1	Hypothetical protein CBG18756 [...	61	2e-07	
gi 16417791 gb AAL18853.1	potassium chloride cotransporter...	60	3e-07	
gi 47202516 emb CAF87431.1	unnamed protein product [Tetrao...	60	3e-07	
gi 4185298 gb AAD09008.1	Na-K-2Cl cotransporter [Rattus no...	60	3e-07	G
gi 16588876 gb AAL26926.1	thiazide-sensitive Na-Cl cotrans...	60	4e-07	
gi 12652805 gb AAH00154.1	SLC12A9 protein [Homo sapiens]	59	6e-07	G
gi 50750706 ref XP_422105.1	PREDICTED: similar to solute c...	59	6e-07	G
gi 38107570 gb EAA53722.1	hypothetical protein MG09472.4 [...	59	6e-07	G
gi 37906389 gb AAP44496.1	Na-K-Cl cotransporter [Aedes aeg...	59	6e-07	
gi 38569457 ref NP_078904.3	solute carrier family 12, memb...	59	8e-07	G
gi 21666316 gb AAM73657.1	solute carrier family 12 member ...	59	8e-07	G
gi 28628359 gb AAQ49174.1	cation-chloride cotransporter 9 ...	59	8e-07	G
gi 47209879 emb CAF91324.1	unnamed protein product [Tetrao...	59	1e-06	
gi 15281553 gb AAK94307.1	solute carrier family 12 member ...	57	2e-06	G
gi 51476920 emb CAH18426.1	hypothetical protein [Homo sapi...	57	2e-06	
gi 31216859 ref XP_316315.1	ENSANGP00000020551 [Anopheles ...	57	3e-06	G
gi 40741631 gb EAA60821.1	hypothetical protein AN4478.2 [A...	57	3e-06	G
gi 33589522 gb AAQ22528.1	LD15480p [Drosophila melanogaste...	57	4e-06	G
gi 33327540 gb AAQ09093.1	SLC12A8 cation-chloride cotransp...	55	8e-06	G
gi 3127109 gb AAC16048.1	Na-K-Cl cotransporter BSC2 [Rattu...	52	7e-05	G

gi 15789485 ref NP_279309.1	cationic amino acid transporte...	52	1e-04	<b>G</b>
gi 79644 pir  S06903	hypothetical protein 128 - Synechococc...	51	2e-04	
gi 26342949 dbj BAC35131.1	unnamed protein product [Mus mu...	50	4e-04	<b>G</b>
gi 31321986 gb AAM48576.1	RHAG-2 [Takifugu rubripes]	50	5e-04	<b>G</b>
gi 21226632 ref NP_632554.1	Amino acid permease [Methanosa...	46	0.005	<b>G</b>
gi 26992100 gb AAN86742.1	Na-K-Cl cotransporter homolog [R...	46	0.005	
gi 47216974 emb CAG04916.1	unnamed protein product [Tetrao...	45	0.011	
gi 47201162 emb CAF87719.1	unnamed protein product [Tetrao...	45	0.011	
gi 31874120 emb CAD97969.1	hypothetical protein [Homo sapi...	42	0.074	<b>G</b>
gi 6324649 ref NP_014718.1	t-SNARE that resides on the end...	42	0.096	<b>G</b>
gi 16903173 gb AAK01946.1	K-Cl cotransporter [Homo sapiens]	40	0.37	<b>G</b>
gi 4584408 emb CAB40707.1	apical Na(2Cl)K cotransporter [B...	39	0.62	<b>G</b>
gi 48840136 ref ZP_00297064.1	COG0531: Amino acid transpor...	39	0.81	
gi 16801675 ref NP_471943.1	similar to amino acid transpor...	39	0.81	<b>G</b>
gi 15922144 ref NP_377813.1	442aa long conserved hypotheti...	37	3.1	<b>G</b>
gi 50753376 ref XP_413964.1	PREDICTED: similar to bumetani...	37	3.1	<b>G</b>
gi 14521274 ref NP_126749.1	hypothetical protein PAB0712 [...	37	4.0	<b>G</b>
gi 46906258 ref YP_012647.1	membrane protein, putative [Li...	37	4.0	<b>G</b>
gi 45519701 ref ZP_00171252.1	COG2244: Membrane protein in...	37	4.0	
gi 24374728 ref NP_718771.1	flagellar biosynthetic protein...	36	5.3	<b>G</b>
gi 33236849 gb AAP98936.1	putative transport permease [Chl...	36	5.3	<b>G</b>
gi 52009842 ref ZP_00337204.1	COG4177: ABC-type branched-c...	36	5.3	
gi 48862094 ref ZP_00315992.1	COG0167: Dihydroorotate dehy...	36	6.9	
gi 20089515 ref NP_615590.1	antigen [Methanosarcina acetiv...	36	6.9	<b>G</b>
gi 45382387 ref NP_990203.1	SOCS box-containing WD protein...	36	6.9	<b>G</b>
gi 50411673 ref XP_457068.1	unnamed protein product [Debar...	36	6.9	<b>G</b>
gi 47095094 ref ZP_00232706.1	membrane protein, putative [...	36	6.9	
gi 20143912 ref NP_599027.1	WD SOCS-box protein 1 isoform ...	35	9.0	<b>G</b>
gi 18677720 ref NP_056441.6	WD SOCS-box protein 1 isoform ...	35	9.0	<b>G</b>
gi 22760676 dbj BAC11291.1	unnamed protein product [Homo s...	35	9.0	<b>G</b>
gi 47096061 ref ZP_00233662.1	amino acid permease family p...	35	9.0	
gi 6563198 gb AAF17193.1	WSB-1 protein [Homo sapiens] >gi ...	35	9.0	<b>G</b>

## Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|22416427|gb|AAM96215.1| **G** potassium-chloride transporter-3a [Homo sapiens]  
gi|5106523|gb|AAD39742.1| **G** K-Cl cotransporter KCC3a [Homo sapiens]  
gi|27151690|sp|Q9UHW9|S126 HUMAN **G** Solute carrier family 12 member 6 (Electroneut  
cotransporter 3) (K-Cl cotransporter 3)  
Length = 1150

Score = 1226 bits (3173), Expect = 0.0

Identities = 835/1350 (61%), Positives = 842/1350 (62%), Gaps = 395/1350 (29%)

Query: 1 MHPPETTTKMASVRFMTPTKIDDIPGLXXXXXXXXXXXXXXXXXXXXXXXXTSRXXXX 60  
MHPPETTTKMASVRFMTPTKIDDIPGL TSR  
Sbjct: 1 MHPPETTTKMASVRFMTPTKIDDIPGLSDTSPDLSSRSSSRVRFSSRESVPETSRS--- 57

```

Query: 61  XXXXXXXXXXXLSQNSGHHKAEGDEYMDTRPGATTSLATVAL-----RTSHPQDVIED----- 111
              E M      GATTSLATVAL      RTSHPQDVIED
Sbjct: 58  -----EPMSEMGATTSLATVALDPPSDRTSHPQDVIEDLSQN 95

Query: 112  -ITGEHSQLLDD-----QRNAYLNNSNYELFEEESFDKNLA-----KVSSLLNRMA 156
              ITGEHSQLLDD      RNAYLNNSNYE  +E FDKNLA      KVSSLLNRMA
Sbjct: 96  SITGEHSQLLDDGHKKARNAYLNNSNYEE-GDEYFDKNLALFEEEMDTRPKVSSLLNRMA 154

Query: 157  NY-----QGAKEHEEAENITNLXXXXXXXXXXXXXQMG-----LQNI FGVT FMGVYILFLRL 207
              NY      QGAKEHEEAENIT      MG      LQNI FG V      ILFLRL
Sbjct: 155  NYTNLTQGAKEHEEAENITEGKKKPTKTPQMGT FMGVYLPCLQNI FG V-----ILFLRL 208

Query: 208  LPCTWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLG 267
              TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP
Sbjct: 209  ---TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP--- 262

Query: 268  TTFEIFLVYEF GGA VGLCF-----AAAMYILGAI-----IVPRAAIFHSDDALKESAA 315
              EFGGAVGLCF      AAAMYILGAI      IVPRAAIFHSDDALKESAA
Sbjct: 263  -----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDALKESAA 313

Query: 316  MLNNMRVYGT AFLVLMVLVVF IG VRYVNKFASXFLACVIVSILAIYAGAIKSSFAPPHFP 375
              MLNNMRVYGT AFLVLMVLVVF IG VRYVNKFAS FLACVIVSILAIYAGAIKSSFAPPHFP
Sbjct: 314  MLNNMRVYGT AFLVLMVLVVF IG VRYVNKFASLFLACVIVSILAIYAGAIKSSFAPPHFP 373

Query: 376  VCMLGNRTLSS--IDVCSKTKEINNMT RHVPSK-----NATCDECNSSYFVHN 421
              VCMLGNRTLSS IDVCSKTKEINNMT VPSK      NATCDE      YFVHN
Sbjct: 374  VCMLGNRTLSSRHIDVCSKTKEINNMT--VPSKLWGFFCNSSQFFNATCDE----YFVHN 427

Query: 422  NVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIE----KSSDVLGSLNHEYVLVDPSAK 477
              NV      TSIQGIPGLASGIITENLWSNYLPKGEIIE      KSSDVLGSLNHEYVLVD
Sbjct: 428  NV---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLVD---- 480

Query: 478  ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTSLWGFF FVYLSNV 537
              ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS      FVYLSNV
Sbjct: 481  ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS-----FVYLSNV 535

Query: 538  VLFGACIEGVVLRDKFG-----VGTLSWP-----SFFSTCGAGDAVKGNLVPWV 581
              VLFGACIEGVVLRDKFG      VGTLSWP      SFFSTCGAG
Sbjct: 536  VLFGACIEGVVLRDKFGDAVKGNLVVGTLSWPSPWVIVIGSFFSTCGAG----- 584

Query: 582  IVIGSLQSLDNIITGAPPFLRWALLRLQAIK-----VFGHSKANGEPT----- 626
              LQSL      TGAP      RLLQAIK      VFGHSKANGEPT
Sbjct: 585  -----LQSL-----TGAP-----RLLQAIKDNIIIPFLRVFGHSKANGEPTWALLLTA 627

Query: 627  -----GILIASLD-----FFLMCYLFTLLRLTAALVAPIAELILSMCALQ----- 666
              GILIASLD      FFLMCYLF L      CALQ
Sbjct: 628  AIAELGILIASLDLVAPILSMFFLMCYLFVN-----ACALQTLLRTPN 671

Query: 667  -----RYYHWALSFMG MTPNWNLARPRPRFSICLALMF-----IVAMVIAGMIGA EK 714
              RYYHWALSFMG M      SICLALMF      IVAMVIAGM
Sbjct: 672  WRPRFRYYHWALSFMG M-----SICLALMFISSWYYAIVAMVIAGM----- 712

Query: 715  SSWYYAIYKXIEYQSLSPHTDEDEWGDGI---XXXXXXXXXXXXXEEGP---KNWRPQXXX 768
              IYK IEYQ      E EWGDGI      EEGP      KNWRPQ
Sbjct: 713  -----IYKIEYQGA-----EKEWGDGIRGLSLSAARFALLRLEEGPPHTKNWRPQLLV 761

Query: 769  XXXXXX-----XXXTFASQLKGNFLHV KAGKGXTIVGSVIV-----GEALAAEQTI 814
              TFASQL      KAGKG TIVGSVIV      GEALAAEQTI
Sbjct: 762  LLKLDEDLHV KHPRLLT FASQL-----KAGKGLTIVGSVIVGNFLENYGEALAAEQTI 814

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Query: 815 KHVACGLLENYLMEAEKVKGFCQL---AKLREGISH-----GGMKHNTVVLIQSMGW 864  
 KH LMEAEKVKGFCQL AKLREGISH GGMKHNTVV MGW  
 Sbjct: 815 KH-----LMEAEKVKGFCQLVVAAKLREGISHLIQSCGLGGMKHNTVV----MGW 860

Query: 865 PNGWRQSERVTTDARAWKTFIGTVKNINIDLFFAAHLALLVA---SFFPSNVEQFSEG-- 919  
 PNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSNVEQFSEG  
 Sbjct: 861 PNGWRQSE---DARAWKTFIGTVR-----VTTAAHLALLVAKNISFFPSNVEQFSEGN 911

Query: 920 -VWWIVHDGGMLML---LLKQHKVWRK-----TVAQLEDNSISCSIQMKATFLYHLRIE 969  
 VWWIVHDGGMLML LLKQHKVWRK TVAQLEDNSI + ATFLYHLRIE  
 Sbjct: 912 DVWWIVHDGGMLMLLPFLLKQHKVWRKCSIRIFTVAQLEDNSIQMKKDL-ATFLYHLRIE 970

Query: 970 AEVRIFKDLEVVRTLEMHSDISAYTYERHMRLSKMMEQRSQML-----TERDRIAQL 1022  
 AEV + +EMHSDISAYTYER + MMEQRSQML TERDR AQL  
 Sbjct: 971 AEVEV-----VEMHSDISAYTYERTL---MMEQRSQMLRHMRLSKTERDREAQL 1017

Query: 1023 VKDRNSMLRLTSIGSXXXXXXXXXXXXXXXXXMAQDLLHTAVYQEKVHM-----SRGQ 1073  
 VKDRNSMLRLTSIGS T YQEKVHM SRGQ  
 Sbjct: 1018 VKDRNSMLRLTSIGSDEDE-----ETETYQEKVHMTWTKDKYMASRGQ 1060

Query: 1074 KAKSMEGF----NMRPDQSNVRRM---KLNEVIVNKSHEAKLVLLNMPGPPRNPEGDEN 1125  
 KAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNMPGPPRNPEGDEN  
 Sbjct: 1061 KAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNMPGPPRNPEGDEN 1120

Query: 1126 YMEFLEVLTXXXXXXXXXXXXXXSEVITIYS 1155  
 YMEFLEVL SEVITIYS  
 Sbjct: 1121 YMEFLEVLTEGLERVLLVRGGGSEVITIYS 1150

☐ >gi|6693798|gb|AAF24986.1| ☒ K-C1 cotransporter KCC3 [Homo sapiens]  
 Length = 1150

Score = 1226 bits (3173), Expect = 0.0  
 Identities = 835/1350 (61%), Positives = 842/1350 (62%), Gaps = 395/1350 (29%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLXXXXXXXXXXXXXXXXXXXXXXXXTSRXXXX 60  
 MHPPETTTKMASVRFMVTPTKIDDIPGL TSR  
 Sbjct: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDLSSRSSRVRFSSRESVPETSRS--- 57

Query: 61 XXXXXXXXXXXLSQNSGHKKAEGDEYMDTRPGATTSLATVAL-----RTSHPQDVIED---- 111  
 E M GATTSLATVAL RTSHPQDVIED  
 Sbjct: 58 -----EPMSEMSGATTSLATVALDPPSDRTSHPQDVIEDLSQN 95

Query: 112 -ITGEHSQLLDD----QRNAYLNNSNYELFEEESFDKNLA-----KVSSLLNRMA 156  
 ITGEHSQLLDD RNAYLNNSNYE +E FDKNLA KVSSLLNRMA  
 Sbjct: 96 SITGEHSQLLDDGHKKARNAYLNNSNYEE-GDEYFDKNLALFEEEMDTRPKVSSLLNRMA 154

Query: 157 NY----QGAKEHEEAENITNLXXXXXXXXXXXXXQMG-----LQNI FGVTFMGVYILFLRL 207  
 NY QGAKEHEEAENIT MG LQNI FGVT FMGVYILFLRL  
 Sbjct: 155 NYTNLTQGAKEHEEAENITEGKKKPTKTPQMGTFMGVYLPCLQNI FGVT----ILFLRL 208

Query: 208 LPCTWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYL 267  
 TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP  
 Sbjct: 209 ---TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP--- 262

Query: 268 TTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDALKESAA 315  
 EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDALKESAA  
 Sbjct: 263 -----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDALKESAA 313



Query: 316 MLNNMRVYGTAFVLMLVLFVFIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFAPPHFP 375  
MLNNMRVYGTAFVLMLVLFVFIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFAPPHFP  
Sbjct: 314 MLNNMRVYGTAFVLMLVLFVFIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFAPPHFP 373

Query: 376 VCMLGNRTLSS--IDVCSKTKEINNMT--VPSK-----NATCDECNSSYFVHN 421  
VCMLGNRTLSS IDVCSKTKEINNMT VPSK NATCDE YFVHN  
Sbjct: 374 VCMLGNRTLSSRHIDVCSKTKEINNMT--VPSKLWGFFCNSSQFFNATCDE----YFVHN 427

Query: 422 NVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIE---KSSDVLGSLNHEYVLVDPSAK 477  
NV TSIQGIPGLASGIITENLWSNYLPKGEIIE KSSDVLGSLNHEYVLVD  
Sbjct: 428 NV---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLVD---- 480

Query: 478 ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS LWGFFFVYLSNV 537  
ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS FVYLSNV  
Sbjct: 481 ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS-----FVYLSNV 535

Query: 538 VLFGACIEGVVLRDKFG-----VGTLSWP-----SFFSTCGAGDAVKGNLVPWV 581  
VLFGACIEGVVLRDKFG VGTLSWP SFFSTCGAG  
Sbjct: 536 VLFGACIEGVVLRDKFGDAVKGNLVVGTLSWPSPWVIVIGSFFSTCGAG----- 584

Query: 582 IVIGSLQSLDNIITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT----- 626  
LQSL TGAP RLLQAIK VFGHSKANGEPT  
Sbjct: 585 -----LQSL-----TGAP-----RLLQAIKDNIIIPFLRVFGHSKANGEPTWALLTA 627

Query: 627 -----GILIASLD-----FFLMCYLFTLLRLTAALVAPIAELILSMCALQ----- 666  
GILIASLD FFLMCYLF L CALQ  
Sbjct: 628 AIAELGILIASLDLVAPILSMFFLMCYLFVN-----ACALQTLRLTPN 671

Query: 667 -----RYYHWALSFMGMTPNWVNLARPRPRFSICLALMF-----IVAMVIAGMIGAEK 714  
RYYHWALSFMGM SICLALMF IVAMVIAGM  
Sbjct: 672 WRPRFRYYHWALSFMGM-----SICLALMFISSWYIAIVAMVIAGM----- 712

Query: 715 SSWYYAIYKXIEYQSLSPHTDEDEWGDGI---XXXXXXXXXXXXXEEGP---KNWRPQXXX 768  
IYK IEYQ E EWGDGI EEGP KNWRPQ  
Sbjct: 713 -----IYKYIEYQGA-----EKEWGDGIRGLSLSAARFALLRLEEGPPHTKNWRPQLLV 761

Query: 769 XXXXXX-----XXXTFASQLKGNFLHVKGKXTIVGSVIV-----GEALAAEQTI 814  
TFASQL KAGKG TIVGSVIV GEALAAEQTI  
Sbjct: 762 LLKLDEDLHVKHPRLLTFASQL-----KAGKGLTIVGSVIVGNFLHNYGEALAAEQTI 814

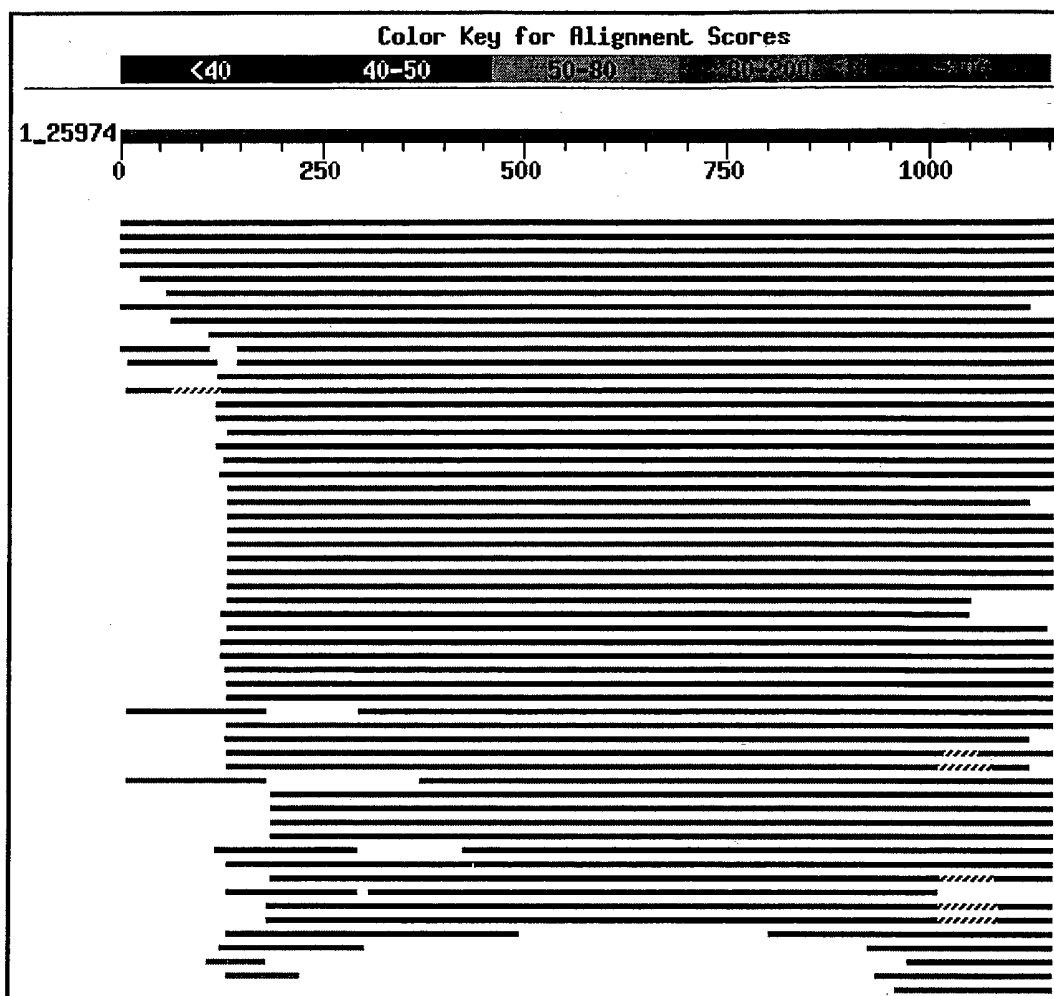
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KH LMEAEKVKGFCQL AKLREGISH GGMKHNTVV MGW  
Sbjct: 815 KH-----LMEAEKVKGFCQLVVA AKLREGISHLIQSCGLGGMKHNTVV----MGW 860

Query: 865 PNGWRQSERVTTDARAWKTFIGTVKNINIDL PFAAHLALLVA---SFFPSNVEQFSEG-- 919  
PNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSNVEQFSEG  
Sbjct: 861 PNGWRQSE----DARAWKTFIGTVR-----VTTAAHLALLVAKNISFFPSNVEQFSEGN 911

Query: 920 -VWWIVHDGGMMLL---LLKQHKVWRK-----TVAQLEDNSISCSIQMKATFLYHLRIE 969  
VWWIVHDGGMMLL LLKQHKVWRK TVAQLEDNSI + ATFLYHLRIE  
Sbjct: 912 DVWWIVHDGGMMLLPFLLLKQHKVWRKCSIRIFTVAQLEDNSIQMKKDL-ATFLYHLRIE 970

Query: 970 AEVRIKFDLEVVRTLEMHDSISAYTYERHMRLSKMMEQRSQML-----TERDRIAQL 1022  
AEV + +EMHDSISAYTYER + MMEQRSQML TERDR AQL  
Sbjct: 971 AEVEV-----VEMHDSISAYTYERTL---MMEQRSQMLRHMRLSKTERDREAQL 1017

Query: 1023 VKDRNSMLRLTSIGSXXXXXXXXXXXXXXXXXMAQDLLHTAVYQEKVHM-----SRGQ 1073  
VKDRNSMLRLTSIGS T YQEKVHM SRGQ  
Sbjct: 1018 VKDRNSMLRLTSIGSDEDE-----ETETYQEKVHMTWTKDKYMASRGQ 1060



## Sequences producing significant alignments:

		Score	E	
		(bits)	Value	
<a href="#">gi 22416427 gb AAM96215.1 </a>	potassium-chloride transporter-3...	<a href="#">2531</a>	0.0	<b>G</b>
<a href="#">gi 6693798 gb AAF24986.1 </a>	K-Cl cotransporter KCC3 [Homo sap...	<a href="#">2531</a>	0.0	<b>G</b>
<a href="#">gi 33329252 gb AAQ10026.1 </a>	K-Cl cotransporter KCC3a-X2M iso...	<a href="#">2499</a>	0.0	<b>G</b>
<a href="#">gi 41281645 ref NP_598410.1 </a>	solute carrier family 12, memb...	<a href="#">2466</a>	0.0	<b>G</b>
<a href="#">gi 47124056 gb AAH70107.1 </a>	SLC12A6 protein [Homo sapiens]	<a href="#">2444</a>	0.0	<b>G</b>
<a href="#">gi 33329256 gb AAQ10028.1 </a>	K-Cl cotransporter KCC3a-S2 isof...	<a href="#">2350</a>	0.0	<b>G</b>
<a href="#">gi 38565928 gb AAH62099.1 </a>	Unknown (protein for MGC:69652) ...	<a href="#">2345</a>	0.0	
<a href="#">gi 22416428 gb AAM96216.1 </a>	potassium-chloride transporter-3...	<a href="#">2294</a>	0.0	<b>G</b>
<a href="#">gi 19526769 ref NP_598409.1 </a>	solute carrier family 12, memb...	<a href="#">2246</a>	0.0	<b>G</b>
<a href="#">gi 19110891 gb AAL85335.1 </a>	K-Cl cotransporter KCC3 variant ...	<a href="#">2221</a>	0.0	<b>G</b>
<a href="#">gi 7512561 pir  T17275</a>	hypothetical protein DKFZp434D2135.1...	<a href="#">2221</a>	0.0	<b>G</b>
<a href="#">gi 34856648 ref XP_342490.1 </a>	similar to K-Cl cotransporter ...	<a href="#">2212</a>	0.0	<b>G</b>
<a href="#">gi 47213488 emb CAF91145.1 </a>	unnamed protein product [Tetrao...	<a href="#">1646</a>	0.0	
<a href="#">gi 9507107 ref NP_062102.1 </a>	solute carrier family 12, membe...	<a href="#">1620</a>	0.0	<b>G</b>
<a href="#">gi 6677993 ref NP_033221.1 </a>	solute carrier family 12, membe...	<a href="#">1614</a>	0.0	<b>G</b>
<a href="#">gi 47522728 ref NP_999114.1 </a>	K-Cl cotransporter [Sus scrofa...	<a href="#">1611</a>	0.0	<b>G</b>

gi 45219767 gb AAH66872.1	Solute carrier family 12, member...	1611	0.0	G
gi 27151684 sp Q28677 S124	RABIT Solute carrier family 12 m...	1608	0.0	
gi 31324218 gb AAP47188.1	potassium-chloride cotransporter...	1607	0.0	G
gi 4827006 ref NP_005063.1	solute carrier family 12 (potas...	1602	0.0	G
gi 3015641 gb AAC39685.1	erythroid K:Cl cotransporter spli...	1511	0.0	G
gi 19705463 ref NP_599190.1	solute carrier family 12 membe...	1431	0.0	G
gi 11968148 ref NP_065759.1	solute carrier family 12 membe...	1426	0.0	G
gi 14193696 gb AAK56093.1	K-Cl cotransporter [Mus musculus...	1426	0.0	G
gi 33859680 ref NP_065066.1	solute carrier family 12, memb...	1426	0.0	G
gi 12003227 gb AAG43493.1	electroneutral potassium-chlorid...	1426	0.0	G
gi 28972652 dbj BAC65742.1	mKIAA1176 protein [Mus musculus]	1426	0.0	G
gi 3015639 gb AAC39684.1	erythroid K:Cl cotransporter spli...	1415	0.0	G
gi 50753670 ref XP_414082.1	PREDICTED: similar to K-Cl cot...	1413	0.0	G
gi 6330233 dbj BAA86490.1	KIAA1176 protein [Homo sapiens]	1398	0.0	G
gi 5730043 ref NP_006589.1	solute carrier family 12 (potas...	1378	0.0	G
gi 47225214 emb CAF98841.1	unnamed protein product [Tetrao...	1374	0.0	
gi 50733496 ref XP_418891.1	PREDICTED: similar to mFLJ0009...	1373	0.0	G
gi 6755534 ref NP_035520.1	solute carrier family 12, membe...	1365	0.0	G
gi 47847414 dbj BAD21379.1	mFLJ00098 protein [Mus musculus]	1365	0.0	G
gi 9651224 gb AAF91094.1	K-Cl cotransporter KCC1 [Mus musc...	1339	0.0	G
gi 32490535 gb AAP84988.1	potassium-chloride cotransporter...	1318	0.0	
gi 47213000 emb CAF95392.1	unnamed protein product [Tetrao...	1147	0.0	
gi 47220725 emb CAG11794.1	unnamed protein product [Tetrao...	1136	0.0	
gi 47223173 emb CAG11308.1	unnamed protein product [Tetrao...	1113	0.0	
gi 10440500 dbj BAB15783.1	FLJ00098 protein [Homo sapiens]	999	0.0	G
gi 21429886 gb AAM50621.1	GH09271p [Drosophila melanogaste...	985	0.0	G
gi 24762439 ref NP_726378.1	CG5594-PA [Drosophila melanoga...	985	0.0	G
gi 46409210 gb AAS93762.1	LD02554p [Drosophila melanogaste...	974	0.0	G
gi 22026947 ref NP_571976.2	CG5594-PC [Drosophila melanoga...	974	0.0	G
gi 10440514 dbj BAB15787.1	FLJ00105 protein [Homo sapiens]	954	0.0	G
gi 34853395 ref XP_217744.2	similar to putative potassium-...	893	0.0	G
gi 48096020 ref XP_394587.1	similar to CG5594-PC [Apis mel...	843	0.0	G
gi 31226974 ref XP_317803.1	ENSANGP00000014479 [Anopheles ...	644	0.0	G
gi 25149428 ref NP_500910.2	solute carrier family 12 membe...	584	e-165	G
gi 39584234 emb CAE61609.1	Hypothetical protein CBG05529 [...	578	e-163	
gi 13507237 gb AAK28520.1	K-Cl cotransporter [Xenopus laevis]	552	e-155	
gi 26343083 dbj BAC35198.1	unnamed protein product [Mus mu...	490	e-136	
gi 32484273 gb AAH54325.1	LOC398663 protein [Xenopus laevis]	474	e-132	G
gi 15208177 dbj BAB63113.1	hypothetical protein [Macaca fa...	439	e-121	
gi 31226957 ref XP_317800.1	ENSANGP00000004794 [Anopheles ...	421	e-115	G
gi 47203569 emb CAG13773.1	unnamed protein product [Tetrao...	389	e-106	
gi 9651629 gb AAF91220.1	potassium-chloride cotransporter ...	375	e-102	
gi 18073139 emb CAC80545.1	putative Na-K-Cl cotransporter ...	365	5e-99	
gi 38073246 gb AAR10807.1	K-Cl cotransporter KCC3a isoform...	356	4e-96	
gi 17541928 ref NP_501141.1	solute carrier family 12 membe...	329	5e-88	G
gi 35505532 gb AAH57624.1	Slc12a5 protein [Mus musculus]	326	4e-87	G
gi 38073248 gb AAR10808.1	brain-specific K-Cl cotransporte...	324	2e-86	
gi 39596034 emb CAE67537.1	Hypothetical protein CBG13060 [...	296	3e-78	
gi 9651216 gb AAF91090.1	K-Cl cotransporter [Mus musculus]	284	2e-74	G

<a href="#">gi 47193414 emb CAG14039.1 </a>	unnamed protein product [Tetrao...	<a href="#">283</a>	4e-74	
<a href="#">gi 7512576 pir  T17231</a>	hypothetical protein DKFZp434F076.1 ...	<a href="#">279</a>	4e-73	<b>G</b>
<a href="#">gi 3925714 emb CAA09464.1 </a>	KCC2 protein [Mus musculus]	<a href="#">267</a>	2e-69	<b>G</b>
<a href="#">gi 3582769 gb AAC35282.1 </a>	erythrocyte K-Cl cotransporter [H...	<a href="#">262</a>	6e-68	<b>G</b>
<a href="#">gi 31226979 ref XP_317804.1 </a>	ENSANGP00000024771 [Anopheles ...	<a href="#">261</a>	2e-67	<b>G</b>
<a href="#">gi 14043556 gb AAH07760.1 </a>	SLC12A7 protein [Homo sapiens]	<a href="#">252</a>	6e-65	<b>G</b>
<a href="#">gi 17534831 ref NP_495555.1 </a>	Na-K-Cl cotransporter (2H716) ...	<a href="#">236</a>	3e-60	<b>G</b>
<a href="#">gi 31226967 ref XP_317802.1 </a>	ENSANGP00000015001 [Anopheles ...	<a href="#">230</a>	3e-58	<b>G</b>
<a href="#">gi 34857570 ref XP_345417.1 </a>	similar to K-Cl cotransporter ...	<a href="#">229</a>	5e-58	<b>G</b>
<a href="#">gi 37575103 gb AAQ93478.1 </a>	furosemide-sensitive KCl cotrans...	<a href="#">221</a>	2e-55	
<a href="#">gi 1673531 gb AAB18960.1 </a>	furosemide-sensitive K-Cl cotrans...	<a href="#">217</a>	2e-54	
<a href="#">gi 39593544 emb CAE61836.1 </a>	Hypothetical protein CBG05808 [...	<a href="#">216</a>	3e-54	
<a href="#">gi 50778569 ref XP_427392.1 </a>	PREDICTED: similar to solute c...	<a href="#">191</a>	2e-46	<b>G</b>
<a href="#">gi 38073244 gb AAR10806.1 </a>	K-Cl cotransporter KCC3b isoform...	<a href="#">167</a>	3e-39	
<a href="#">gi 30691724 ref NP_849732.1 </a>	cation-chloride cotransporter,...	<a href="#">138</a>	1e-30	<b>G</b>
<a href="#">gi 34905658 ref NP_914176.1 </a>	putative cation-chloride co-tr...	<a href="#">134</a>	3e-29	<b>G</b>
<a href="#">gi 50944163 ref XP_481609.1 </a>	putative Na+/K+/Cl-cotransport...	<a href="#">133</a>	5e-29	
<a href="#">gi 52075682 dbj BAD44902.1 </a>	putative potassium-chloride cot...	<a href="#">132</a>	9e-29	
<a href="#">gi 16417791 gb AAL18853.1 </a>	potassium chloride cotransporter...	<a href="#">131</a>	2e-28	
<a href="#">gi 2582381 gb AAC49874.1 </a>	cation-chloride co-transporter [N...	<a href="#">123</a>	4e-26	
<a href="#">gi 20151457 gb AAM11088.1 </a>	GH27027p [Drosophila melanogaste...	<a href="#">118</a>	1e-24	<b>G</b>
<a href="#">gi 31242251 ref XP_321556.1 </a>	ENSANGP00000011560 [Anopheles ...	<a href="#">118</a>	2e-24	<b>G</b>
<a href="#">gi 516001 gb AAC48592.1 </a>	bumetanide-sensitive Na-K-Cl cotra...	<a href="#">112</a>	1e-22	
<a href="#">gi 1079521 gb AAC52633.1 </a>	kidney-specific Na-K-Cl cotranspo...	<a href="#">112</a>	1e-22	<b>G</b>
<a href="#">gi 2290526 gb AAB65150.1 </a>	Na-(K)-Cl cotransporter isoform m...	<a href="#">112</a>	1e-22	<b>G</b>
<a href="#">gi 21686589 gb AAM74968.1 </a>	renal Na-K-Cl cotransporter isof...	<a href="#">111</a>	2e-22	
<a href="#">gi 21686587 gb AAM74967.1 </a>	renal Na-K-Cl cotransporter isof...	<a href="#">111</a>	2e-22	
<a href="#">gi 25304083 gb AAH40138.1 </a>	Unknown (protein for MGC:48843) ...	<a href="#">109</a>	7e-22	
<a href="#">gi 6755532 ref NP_035519.1 </a>	solute carrier family 12, membe...	<a href="#">109</a>	7e-22	<b>G</b>
<a href="#">gi 34365781 ref NP_899197.1 </a>	solute carrier family 12, memb...	<a href="#">109</a>	7e-22	<b>G</b>
<a href="#">gi 16877251 gb AAH16888.1 </a>	Solute carrier family 12, member...	<a href="#">109</a>	7e-22	<b>G</b>
<a href="#">gi 27151793 sp P55014 S121</a>	MOUSE Solute carrier family 12 m...	<a href="#">109</a>	7e-22	<b>G</b>
<a href="#">gi 40950187 gb AAR97733.1 </a>	Na-K-Cl cotransporter [Oreochrom...	<a href="#">109</a>	7e-22	
<a href="#">gi 9507103 ref NP_062007.1 </a>	solute carrier family 12, membe...	<a href="#">108</a>	2e-21	<b>G</b>
<a href="#">gi 38073242 gb AAR10805.1 </a>	K-Cl cotransporter KCC4 [Rattus ...	<a href="#">107</a>	4e-21	<b>G</b>

#### Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|22416427|gb|AAM96215.1|](#) **G** potassium-chloride transporter-3a [Homo sapiens]  
[gi|5106523|gb|AAD39742.1|](#) **G** K-Cl cotransporter KCC3a [Homo sapiens]  
[gi|27151690|sp|Q9UHW9|S126](#) HUMAN **G** Solute carrier family 12 member 6 (Electroneut  
cotransporter 3) (K-Cl cotransporter 3)  
Length = 1150

Score = 2531 bits (5961), Expect = 0.0

Identities = 926/1362 (67%), Positives = 930/1362 (68%), Gaps = 419/1362 (30%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDXSSRSSSRVRFSSRESVPETSRSEPM 60  
 MHPPE...T...K...M...S...V...R...F...M...T...P...T...K...I...D...I...P...G...L...S...D...T...S...P...D...X...S...S...R...S...S...R...V...R...F...S...S...R...E...S...V...P...E...T...S...R...S...E...P...M... 60  
 Sbjct: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDLSSRSSSRVRFSSRESVPETSRSEPM 60

Query: 61 SEMSDPPSDLSONSGHKAEGDEYMDTRPGATTSLATVAL-----RTSHPQDVIED----- 111  
 SEMS GATTSLATVAL RTSHPQDVIED  
 Sbjct: 61 SEMS-----GATTSLATVALDPPSDRTSHPQDVIEDLSQN 95

Query: 112 -ITGEHSQLLDD----QRNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRM 155  
 ITGEHSQLLDD RNAYLNNSNYE E +E FDKNLA KVSSLLNRM  
 Sbjct: 96 SITGEHSQLLDDGHKKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRM 153

Query: 156 ANY----QGAKEHEEAENITNLTTEGKKKPTKTPQMG-----LQNI FGVT FMGVYI 202  
 ANY QGAKEHEEAENIT EGKKKPTKTPQMG LQNI FGVT I  
 Sbjct: 154 ANYTNLTQGAKEHEEAENIT----EGKKKPTKTPQMGT FMGVYLPCLQNI FGVT -----I 203

Query: 203 LFLRLLPCTWVVGTAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 262  
 LFLRL TWVVGTAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL  
 Sbjct: 204 LFLRL---TWVVGTAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 260

Query: 263 GPYLGTTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDAL 310  
 GP EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDAL  
 Sbjct: 261 GP-----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDAL 308

Query: 311 KESAAMLNNMRVYGT AFLVLMVLVVFVIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFA 370  
 KESAAMLNNMRVYGT AFLVLMVLVVFVIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFA  
 Sbjct: 309 KESAAMLNNMRVYGT AFLVLMVLVVFVIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFA 368

Query: 371 PPHFVCM LGNRTLSS--IDVCSKTKEINNMT RHVPSK-----NATCDECNSS 416  
 PPHFVCM LGNRTLSS IDVCSKTKEINNMT VPSK NATCDE  
 Sbjct: 369 PPHFVCM LGNRTLSSRHIDVCSKTKEINNMT--VPSKLWGFFCNSSQFFNATCDE---- 422

Query: 417 YFVHNNVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK----SSDVLGSLNHEYVLV 472  
 YFVHNNV TSIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLGSLNHEYVLV  
 Sbjct: 423 YFVHNNV---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLV 479

Query: 473 DPSAKITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS LWGFFV 532  
 D ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS FV  
 Sbjct: 480 D----ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS-----FV 530

Query: 533 YLSNVVLF GACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIVI 584  
 YLSNVVLF GACIEGVVLRDKFG DAVKGNLV PWVIVI  
 Sbjct: 531 YLSNVVLF GACIEGVVLRDKFG-----DAVKGNLVVGTLSWPSFPWVIVI 574

Query: 585 GS-----LQSLDNIITGAPPFLRWALLRLLQAIK-----VFGH SKANGEPT-- 626  
 GS LQSL TGAP RLLQAIK VFGH SKANGEPT  
 Sbjct: 575 GSFFSTCGAGLQSL---TGAP-----RLLQAIKDNIIIPFLRVFGH SKANGEPTWA 622

Query: 627 -----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----CA 664  
 GILIASLD LVAPI LSM CA  
 Sbjct: 623 LLLTAAIAELGILIASLD-----LVAPI---LSMFFLMCYL FVN LACA 662

Query: 665 LQ-----RYYHWALSFMGMT PNWVN LARPRPRFSICLALMFI-----VAMV 705  
 LQ RYYHWALSFMGM SICLALMFI VAMV  
 Sbjct: 663 LQTLRLTPNWRPRFRYYHWALSFMGM-----SICLALMFISSWYIAIVAMV 708

Query: 706 IAGMIGA EKSSWYIAIYKXIEYQSLSPHTDEDEWGDGIRGL---AARFALLRLEEGP--- 759  
 IAGM IYK IEYQ E EWGDGIRGL AARFALLRLEEGP  
 Sbjct: 709 IAGM-----IYKIEYQG-----AEKEWGDGIRGLSLSAARFALLRLEEGP PHT 752

Query: 760 KNWRPQLLVLLKL-----HPRLLTFASQLKGNFLHVKAGKGXTIVGSVIVG----- 805  
 KNWRPQLLVLLKL HPRLLTFASQLK AGKG TIVGSVIVG  
 Sbjct: 753 KNWRPQLLVLLKLDEDLHVKHPRLLTFASQLK-----AGKGLTIVGSVIVGNFLENYG 805

Query: 806 EALAAEQTIKHVVACGLLENYLMEAEKVKGFCQL---AKLREGISH-----GGMKHNT 855  
 EALAAEQTIKH LMEAEKVKGFCQL AKLREGISH GGMKHNT  
 Sbjct: 806 EALAAEQTIKH-----LMEAEKVKGFCQLVVA AKLREGISHLIQSCGLGGMKHNT 855

Query: 856 VVLIQSMGWPNGWRQSERVTTDARAWKTFIGTVKNINIDL PFAAHLALLVA---SFFPSN 912  
 VV MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSN  
 Sbjct: 856 VV----MGWPNGWRQSE----DARAWKTFIGTVR-VTT----AAHLALLVAKNISFFPSN 902


Query: 913 VEQFSEG---VWWIVHDGGMLMLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK- 959  
 VEQFSEG VWWIVHDGGMLMLL LKQHKVWRK TVAQLEDNSI QMK  
 Sbjct: 903 VEQFSEGNI DVWWIVHDGGMLMLLPFL LKQHKVWRKCSIRIFTVAQLEDNSI----QMKK 958

Query: 960 --ATFLYHLRIEAEVRIKDLLEVVRTLEMHSDISAYTYERHMRSLKMMEQRSQML----- 1013  
 ATFLYHLRIEAEV EVV EMHSDISAYTYER + MMEQRSQML  
 Sbjct: 959 DLATFLYHLRIEAEV-----EVV---EMHSDISAYTYERTL-----MMEQRSQMLRHRMR 1005

Query: 1014 ---TERDRIAQLVKDRNSMLRLTSIGSDEDEETETTTWKDKYMAQDLLHTAVYQEKVHM- 1069  
 TERDR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM  
 Sbjct: 1006 LSKTERDREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHMT 1048

Query: 1070 -----SRGQKAKSMEGF----NMRPDQSNVRRM----KLNEVIVNKSHEAKLVLLNM 1113  
 SRGQKAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNM  
 Sbjct: 1049 WTKDKYMASRGQKAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNM 1108

Query: 1114 PGPPRNPEGDENYMEFLEVLTEGLERVLVLRGGGSEVITIYS 1155  
 PGPPRNPEGDENYMEFLEVLTEGLERVLVLRGGGSEVITIYS  
 Sbjct: 1109 PGPPRNPEGDENYMEFLEVLTEGLERVLVLRGGGSEVITIYS 1150

☐ >gi|6693798|gb|AAF24986.1|  K-C1 cotransporter KCC3 [Homo sapiens]  
 Length = 1150

Score = 2531 bits (5961), Expect = 0.0

Identities = 926/1362 (67%), Positives = 930/1362 (68%), Gaps = 419/1362 (30%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDXSSRSSSRVRFSSRESVPETSRSEPM 60  
 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPD SSRSSSRVRFSSRESVPETSRSEPM  
 Sbjct: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDLSSRSSSRVRFSSRESVPETSRSEPM 60

Query: 61 SEMSDPPSDLSQNSGHKKAEGDEYMDTRPGATTSLATVAL-----RTSHPDVIED---- 111  
 SEMS GATTSLATVAL RTSHPDVIED  
 Sbjct: 61 SEMS-----GATTSLATVALDPPSDRTSHPDVIEDLSQN 95

Query: 112 -ITGEHSQLLDD----QRNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRM 155  
 ITGEHSQLLDD RNAYLNNSNYE E +E FDKNLA KVSSLLNRM  
 Sbjct: 96 SITGEHSQLLDDGHHKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRM 153

Query: 156 ANY----QGAKEHEEAENITNLTTGEGKKKPTKTPQMG-----LQNI FGVTFMGVYI 202  
 ANY QGAKEHEEAENIT EGKKKPTKTPQMG LQNI FG V I  
 Sbjct: 154 ANYTNLTQGAKEHEEAENIT----EGKKKPTKTPQMGT FMGVYLPCLQNI FG V-----I 203

Query: 203 LFLRLLPCTWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 262  
 LFLRL TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL  
 Sbjct: 204 LFLRL---TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 260

Query: 263 GPYLGTTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDAL 310  
 GP EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDAL

Sbjct: 261 GP-----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDAL 308

Query: 311 KESAAMLNNMRVYGTAFVLVLMVLVVFVIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFA 370  
 KESAAMLNNMRVYGTAFVLVLMVLVVFVIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFA

Sbjct: 309 KESAAMLNNMRVYGTAFVLVLMVLVVFVIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFA 368

Query: 371 PPHFVCM LGNRTLSS--IDVCSKTKEINNMT RHVPSK-----NATCDECNSS 416  
 PPHFVCM LGNRTLSS IDVCSKTKEINNMT VPSK NATCDE

Sbjct: 369 PPHFVCM LGNRTLSS RHIDVCSKTKEINNMT--VPSKLWGFFCNSSQFFNATCDE---- 422

Query: 417 YFVHNNVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK----SSDVLGSLNHEYVLV 472  
 YFVHNNV TSIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLGSLNHEYVLV

Sbjct: 423 YFVHNNV---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLV 479

Query: 473 DPSAKITTSFTLLVGIFFPSTVGIMAGSNRSGDLKDAQSIPIGTILAILTTS LWGFFV 532  
 D ITTSFTLLVGIFFPSTVGIMAGSNRSGDLKDAQSIPIGTILAILTTS FV

Sbjct: 480 D----ITTSFTLLVGIFFPSTVGIMAGSNRSGDLKDAQSIPIGTILAILTTS-----FV 530

Query: 533 YLSNVVLF GACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIVI 584  
 YLSNVVLF GACIEGVVLRDKFG DAVKGNLV PWVIVI

Sbjct: 531 YLSNVVLF GACIEGVVLRDKFG-----DAVKGNLVGTLSWPSPWVIVI 574

Query: 585 GS-----LQSLDNIITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT-- 626  
 GS LQSL TGAP RLLQAIK VFGHSKANGEPT

Sbjct: 575 GSFFSTCGAGLQSL----TGAP-----RLLQAIKDNIIIPFLRVFGHSKANGEPTWA 622

Query: 627 -----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----CA 664  
 GILIASLD LVAPI LSM CA

Sbjct: 623 LLLTAAIAELGILIASLD-----LVAPI----LSMFFLMCYLFVNLACA 662

Query: 665 LQ-----RYYHWALSFMGMTPNWVNLRPRPRFSICLALMFI-----VAMV 705  
 LQ RYYHWALSFMGM SICLALMFI VAMV

Sbjct: 663 LQTLRLTPNWRPRFRYYHWALSFMGM-----SICLALMFISSWYYAIVAMV 708

Query: 706 IAGMIGA EKSSWYYAIYKXIEYQSLSPHTDEWDGIRGL---AARFALLRLEEGP--- 759  
 IAGM IYK IEYQ E EWGDGIRGL AARFALLRLEEGP

Sbjct: 709 IAGM-----IYKIEYQG-----AEKEWDGIRGLSLSAARFALLRLEEGPPHT 752

Query: 760 KNWRPQLLVLLKL-----HPRLLT FASQLKGNFLHV KAGKXTIVGSVIVG----- 805  
 KNWRPQLLVLLKL HPRLLT FASQLK AGKG TIVGSVIVG

Sbjct: 753 KNWRPQLLVLLKLDEDLHV KHPRLLT FASQLK-----AGKGLTIVGSVIVGNFLHNYG 805

Query: 806 EALAAEQTIKHVVACGLLENYLMEAEKVKGFCQL---AKLREGISH-----GGMKHNT 855  
 EALAAEQTIKH LMEAEKVKGFCQL AKLREGISH GGMKHNT

Sbjct: 806 EALAAEQTIKH-----LMEAEKVKGFCQLVVA AKLREGISHLIQSCGLGGMKHNT 855

Query: 856 VVLIQSMGWPNGWQSERVTTDARAWKTFIGTVKNINIDL PFAAHLALLVA---SFFPSN 912  
 VV MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSN

Sbjct: 856 VV----MGWPNGWRQSE----DARAWKTFIGTVR-VTT----AAHLALLVAKNISFFPSN 902

Query: 913 VEQFSEG---VWWIVHDGGM LMLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK- 959  
 VEQFSEG VWWIVHDGGM LMLL LKQHKVWRK TVAQLEDNSI QMK

Sbjct: 903 VEQFSEG NIDVWWIVHDGGM LMLLPFL LKQHKVWRKCSIRIFTVAQLEDNSI----QMKK 958

Query: 960 --ATFLYHLRIEAEVRIFKDLEVVRTLEMHDS DISAYTYERHMR LSKMMEQRSQML---- 1013  
 ATFLYHLRIEAEV EVV EMHDS DISAYTYER + MMEQRSQML

Sbjct: 959 DLATFLYHLRIEAEV-----EVV---EMHDS DISAYTYERTL----MMEQRSQMLRHMR 1005

Query: 1014 ---TERDRIAQLVKDRNSMLRLTSIGSDEDEETETTTWKDKYMAQDLLHTAVYQEKVHM- 1069  
 TERDR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM  
 Sbjct: 1006 LSKTERDREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHMT 1048

Query: 1070 -----SRGQKAKSMEGF----NMRPDQSNVRRM----KLNEVIVNKSHEAKLVLLNM 1113  
 SRGQKAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNM  
 Sbjct: 1049 WTKDKYMASRGQKAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNM 1108

Query: 1114 PGPPRNPEGDENYMEFLEVLTEGLERVLVRRGGGSEVITIYS 1155  
 PGPPRNPEGDENYMEFLEVLTEGLERVLVRRGGGSEVITIYS  
 Sbjct: 1109 PGPPRNPEGDENYMEFLEVLTEGLERVLVRRGGGSEVITIYS 1150

☐ >gi|33329252|gb|AAQ10026.1| ☒ K-C1 cotransporter KCC3a-X2M isoform [Homo sapiens]  
 Length = 1135

Score = 2499 bits (5886), Expect = 0.0

Identities = 916/1356 (67%), Positives = 920/1356 (67%), Gaps = 422/1356 (31%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDXSSRSSRVRFSSRESVPETSRSEPM 60  
 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPD SSRSSRVRFSSRESVPETSRSEPM  
 Sbjct: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDLSSRSSRVRFSSRESVPETSRSEPM 60

Query: 61 SEMSDPPSDLSQNSGHKKAEGDEYMDTRPGATTSLATVAL-----RTSHPDQDVIEDITGE 115  
 SEMS GATTSLATVAL RTSHPDQDVIED  
 Sbjct: 61 SEMS-----GATTSLATVALDPPSDRTSHPDQDVIED----- 91

Query: 116 HSQLLDDQ---RNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRMANY--- 158  
 D RNAYLNNSNYE E +E FDKNLA KVSSLLNRMANY  
 Sbjct: 92 -----DGHKKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRMANYTNL 144

Query: 159 -QGAKEHEEAENITNLTTEGKKKPTKTPQMG-----LQNIFGVTFMGVYILFLRL 208  
 QGAKEHEEAENIT EGKKKPTKTPQMG LQNIFGV ILFLRL  
 Sbjct: 145 TQGAKEHEEAENIT---EGKKKPTKTPQMGTFMGVYLPCLQNIFGV-----ILFLRL- 193

Query: 209 PCTWVVGTAGVLQAFIAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLG 268  
 TWVVGTAGVLQAFIAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP  
 Sbjct: 194 --TWVVGTAGVLQAFIAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP---- 247

Query: 269 TFEIFLVYEFEGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDALKESAAM 316  
 EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDALKESAAM  
 Sbjct: 248 -----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDALKESAAM 299

Query: 317 LNNMRVYGTAFVLVLMVLVVFVIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFAPPHFPV 376  
 LNNMRVYGTAFVLVLMVLVVFVIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFAPPHFPV  
 Sbjct: 300 LNNMRVYGTAFVLVLMVLVVFVIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFAPPHFPV 359

Query: 377 CMLGNRTLSS--IDVCSKTKEINNMTTRHVPSK-----NATCDECNSSYFVHNN 422  
 CMLGNRTLSS IDVCSKTKEINNMT VPSK NATCDE YFVHNN  
 Sbjct: 360 CMLGNRTLSSRHIDVCSKTKEINNMT--VPSKLWGFFCNSSQFFNATCDE----YFVHNN 413

Query: 423 VQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK-----SSDVLGSLNHEYVLVDPSAKI 478  
 V TSIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLGSLNHEYVLVD I  
 Sbjct: 414 V---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLVD----I 466

Query: 479 TTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTSWLGFFVYLSNVV 538  
 TTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS FVYLSNVV  
 Sbjct: 467 TTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS-----FVYLSNVV 521



Query: 539 LFGACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIVIGS---- 586  
 LFGACIEGVVLRDKFG DAVKGNLV PWVIVIGS  
 Sbjct: 522 LFGACIEGVVLRDKFG-----DAVKGNLVVGTLSWPSFPWVIVIGSFFST 565

Query: 587 ----LQSLDNIITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT----- 626  
 LQSL TGAP RLLQAIK VFGHSKANGEPT  
 Sbjct: 566 CGAGLQSL----TGAP-----RLLQAIKDNIIIPFLRVFGHSKANGEPTWALLLTAA 613

Query: 627 ----GILIASLDFFFLMCYLFTLLRLTAALVAPIAELILSM-----CALQ----- 666  
 GILIASLD LVAPI LSM CALQ  
 Sbjct: 614 IAEKGILIASLD-----LVAPI----LSMFFFLMCYLFVNACALQTLR 653

Query: 667 -----RYYHWALSFMGMTPNWNLARPRPRFSICLALMFI-----VAMVIAGMIG 711  
 RYYHWALSFMGM SICLALMFI VAMVIAGM  
 Sbjct: 654 TPNWRPRFRYYHWALSFMGM-----SICLALMFISSWYYAIVAMVIAGM-- 697

Query: 712 AEKSSWYYAIYKXIEYQSLSPHTDEDEWGDGIRGL---AARFALLRLEEGP---KNWRPQ 765  
 IYK IEYQ E EWGDGIRGL AARFALLRLEEGP KNWRPQ  
 Sbjct: 698 -----IYKIEYQG-----AEKEWGDGIRGLSLSAARFALLRLEEGPPHTKNWRPQ 743

Query: 766 LLVLLKL-----HPRLLTFASQLKGNFLHVKGKXTIVGSVIVG-----EALAAE 811  
 LLVLLKL HPRLLTFASQLK AGKG TIVGSVIVG EALAAE  
 Sbjct: 744 LLVLLKLDEDLHVKHPRLLTFASQLK-----AGKGLTIVGSVIVGNFLENYGEALAAE 796

Query: 812 QTIKHVVACGLLENYLMEAEKVGKFCQL---AKLREGISH-----GGMKHNTVVLIIQS 861  
 QTIKH LMEAEKVGKFCQL AKLREGISH GGMKHNTVV  
 Sbjct: 797 QTIKH-----LMEAEKVGKFCQLVVAAKLREGISHLIQSCGLGGMKHNTVV---- 842

Query: 862 MGWPNGWRQSERVTTDARAWKTFIGTVKNINIDL PFAAHLALLVA---SFFPSNVEQFSE 918  
 MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSNVEQFSE  
 Sbjct: 843 MGWPNGWRQSE----DARAWKTFIGTVR-VTT---AAHLALLVAKNISFFPSNVEQFSE 893

Query: 919 G---VWWIVHDGGMLMLL---LKQHKVVRK-----TVAQLEDNSISCSIQMK---ATFL 963  
 G VWWIVHDGGMLMLL LKQHKVVRK TVAQLEDNSI QMK ATFL  
 Sbjct: 894 GNIDVWWIVHDGGMLMLLPFLKQHKVVRKCSIRIFTVAQLEDNSI----QMKKDLATFL 949

Query: 964 YHLRIEAEVRIFKDLEVVRTLEMHSDISAYTYERHMRLSKMMEQRSQML-----TER 1016  
 YHLRIEAEV EVV EMHSDISAYTYER + MMEQRSQML TER  
 Sbjct: 950 YHLRIEAEV-----EVV---EMHSDISAYTYERTL----MMEQRSQMLRHMRLSKTER 996

Query: 1017 DRIAQLVKDRNSMLRLTSIGSDEDEETETTTWKDKYMAQDLLHTAVYQEKVHM----- 1069  
 DR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM  
 Sbjct: 997 DREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHMTWTKDKY 1039

Query: 1070 --SRGQKAKSMEGF----NMRPDQSNVRRM----KLNEVIVNKSHEAKLVLLNMPGPPRN 1119  
 SRGQKAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNMPGPPRN  
 Sbjct: 1040 MASRGQKAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNMPGPPRN 1099

Query: 1120 PEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS 1155  
 PEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS  
 Sbjct: 1100 PEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS 1135

☐ >gi|41281645|ref|NP\_598410.1| ☒ solute carrier family 12, member 6 [Mus musculus]  
☒ gi|15042077|gb|AAK81895.1| ☒ K-C1 cotransporter 3a [Mus musculus]  
☒ gi|27151686|sp|Q924N4|S126 MOUSE Solute carrier family 12 member 6 (Electroneutral  
 cotransporter 3) (K-C1 cotransporter 3)  
 Length = 1150

Score = 2466 bits (5808), Expect = 0.0

Identities = 907/1362 (66%), Positives = 923/1362 (67%), Gaps = 419/1362 (30%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDXSSRSSSRVRFSSRESVPETSRSEPM 60  
MHPPE TTKM+SVRFMVTPTKIDDIPGLSDTSPD SSRSSSRVRFSSRESVPETSRSEPM  
Sbjct: 1 MHPPEATTKMSSVRFMVTPTKIDDIPGLSDTSPDLSSRSSSRVRFSSRESVPETSRSEPM 60

Query: 61 SEMSDPPSDLSONSGHKKAEDEYMDTRPGATTSLATVAL-----RTSHPQDVIED---- 111  
SE+S GATTSLATVAL RTS+PQDV ED  
Sbjct: 61 SELS-----GATTSLATVALDPSSDRTSNPQDVTEDPSQN 95

Query: 112 -ITGEHSQLLDD----QRNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRM 155  
ITGEHSQLLDD RNAYLNNSNYE E +E FDKNLA KVSSLLNRM  
Sbjct: 96 SITGEHSQLLDDGHKKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRM 153

Query: 156 ANY----QGAKEHEEAENITNLTTEGKKKPTKTPQMG-----LQNI FGVT FMGVYI 202  
ANY QGAKEHEEAENIT EGKKKPTK+PQMG LQNI FG V I  
Sbjct: 154 ANYTNLTQGAKEHEEAENIT----EGKKKPTKSPQMGT FMGVYLPCLQNI FG V-----I 203

Query: 203 LFLRLLPCTWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 262  
LFLRL TWVVG TAG+LQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL  
Sbjct: 204 LFLRL---TWVVG TAGILQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 260

Query: 263 GPYLGTTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDAL 310  
GP EFGGAVGLCF AAAMYILGAI IVPRAAIF SDDAL  
Sbjct: 261 GP-----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFRSDDAL 308

Query: 311 KESAAMLNNMRVYGTAFLVLMVLVVF IGVRVYNKFASXFLACVIVSILAIYAGAIKSSFA 370  
KESAAMLNNMRVYGTAFLVLMVLVVF IGVRVYNKFAS FLACVIVSILAIYAGAIKSSFA  
Sbjct: 309 KESAAMLNNMRVYGTAFLVLMVLVVF IGVRVYNKFASLFLACVIVSILAIYAGAIKSSFA 368

Query: 371 PPFFPVCMLGNRTLSS--IDVCSKTKEINNMT RHVPSK-----NATCDECNSS 416  
PPFFPVCMLGNRTLSS +D+CSKTKE++NMT VPSK NATCDE  
Sbjct: 369 PPFFPVCMLGNRTLSSRHL DICSKTKEVDNMT--VPSKLWGFCNSSQFFNATCDE---- 422

Query: 417 YFVHNNVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK----SSDVLGSLNHEYVLV 472  
YFVHNNV SIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLG+LNHEYVL  
Sbjct: 423 YFVHNNV---ISIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGNLNHEYVLA 479

Query: 473 DPSAKITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS LWGFFV 532  
D ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS FV  
Sbjct: 480 D----ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS-----FV 530

Query: 533 YLSNVVLF GACIEGVVLRDKFGVGTLSWP SFFSTCGAGDAVKGNLV-----PWVIVI 584  
YLSNVVLF GACIEGVVLRDKFG DAVKGNLV PWVIVI  
Sbjct: 531 YLSNVVLF GACIEGVVLRDKFG-----DAVKGNLVVGTLSWPSPWVIVI 574

Query: 585 GS-----LQSLDNIITGAPFLRWALLRLLQAIK-----VFGH SKANGEPT-- 626  
GS LQSL TGAP RLLQAIK VFGH SKANGEPT  
Sbjct: 575 GSFFSTCGAGLQSL---TGAP-----RLLQAIKDNII PFLRVFGH SKANGEPTWA 622

Query: 627 -----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----CA 664  
GILIASLD LVAPI LSM CA  
Sbjct: 623 LLLTAATAELGILIASLD-----LVAPI----LSMFFLMCYLFVNLACA 662

Query: 665 LQ-----RYYHWALSFMGMT PNWVNLRPRPRFSICLALMFI-----VAMV 705  
LQ RYYHWALSFMGM SICLALMFI VAMV  
Sbjct: 663 LQTLRLTPNWRPRFRYYHWALSFMGM-----SICLALMFISSWYYAIVAMV 708

Query: 706 IAGMIGA EKSSWYIAYIKXIEYQSLSPHTDEDEWGDGIRGL---AARFALLRLEEGP--- 759  
 IAGM IYK IEYQ E EWGDGIRGL AARFALLRLEEGP  
 Sbjct: 709 IAGM-----IYKIEYQG-----AEKEWGDGIRGLSLSAARFALLRLEEGP 752

Query: 760 KNWRPQLLVLLKL-----HPRLLTFASQLKGNFLHV KAGKGXTIVGSVIVG----- 805  
 KNWRPQLLVLLKL HPRLLTFASQLK AGKG TIVGSVIVG  
 Sbjct: 753 KNWRPQLLVLLKLDEDLHV KHPRLTFASQLK-----AGKGLTIVGSVIVGNFLENYG 805

Query: 806 EALAAEQTIKHVACGLLENYLMEAEKVKGFCQL---AKLREGISH-----GGMKHNT 855  
 +ALAAEQTIKH LMEAEKVKGFCQL AKL+EGISH GGMKHNT  
 Sbjct: 806 DALAAEQTIKH-----LMEAEKVKGFCQLVVA AKLKEGISHLIQSCGLGGMKHNT 855

Query: 856 VVLIQSMGWPNGWQRQSERVTTDARAWKTFIGTVKNINIDL PFAAHLALLVA---SFFPSN 912  
 VV MGWPNGWQRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSN  
 Sbjct: 856 VV----MGWPNGWQRQSE----DARAWKTFIGTVR-VTT----AAHLALLVAKNV SFFPSN 902

Query: 913 VEQFSEG---VWWIVHDGGMLMLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK- 959  
 VEQFSEG V WIVHDGGMLMLL LKQHKVWRK TVAQLEDNSI QMK  
 Sbjct: 903 VEQFSEGNIDVRWIVHDGGMLMLLPFL LKQHKVWRKCSIRIFTVAQLEDNSI----QMKK 958

Query: 960 --ATFLYHLRIEAEVRIFKDLEVVRTLEMHDS DISAYTYERHMR LSKMMEQRSQML---- 1013  
 ATFLYHLRIEAEV EVV EMHDS DISAYTYER + MMEQRSQML  
 Sbjct: 959 DLATFLYHLRIEAEV-----EVV---EMHDS DISAYTYERTL----MMEQRSQMLRHMR 1005

Query: 1014 ---TERDRIAQLVKDRNSMLRLTSIGSDEDEETETTWT KD KYMAQDLLHTAVYQEKVHM- 1069  
 TERDR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM  
 Sbjct: 1006 LSKTERDREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHMT 1048

Query: 1070 -----SRGQKAKSMEGF-----NMRPDQSNVRRM----KLNEVIVNKSHEAKLVLLNM 1113  
 SRGQK KSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNM  
 Sbjct: 1049 WTKDKYMASRGQKVKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNM 1108

Query: 1114 PGPPRNPEGDENYMEFLEVLTEGLERVL LVRGGGSEVITIYS 1155  
 PGPPRNPEGDENYMEFLEVLTEGLERVL LVRGGGSEVITIYS  
 Sbjct: 1109 PGPPRNPEGDENYMEFLEVLTEGLERVL LVRGGGSEVITIYS 1150

☐ >gi|47124056|qb|AAH70107.1| **G** SLC12A6 protein [Homo sapiens]  
 Length = 1156

Score = 2444 bits (5755), Expect = 0.0

Identities = 900/1336 (67%), Positives = 904/1336 (67%), Gaps = 419/1336 (31%)

Query: 27 GLSDTSPDXSSRSSSRVRFSSRESVPETSRSEPMSEMSDPPSDLSQNSGHKKAEGDEYMD 86  
 GLSDTSPD SSRSSSRVRFSSRESVPETSRSEPMSEMS  
 Sbjct: 33 GLSDTSPDLSSRSSSRVRFSSRESVPETSRSEPMSEMS----- 70

Query: 87 TRPGATTSLATVAL-----RTSHPQDVIED-----ITGEHSQLLDD----QRNAYLNNSN 132  
 GATTSLATVAL RTSHPQDVIED ITGEHSQLLDD RNAYLNNSN  
 Sbjct: 71 ---GATTSLATVALDPPSDRTSHPQDVIEDLSQNSITGEHSQLLDDGHKKARNAYLNNSN 127

Query: 133 YELFE-EESFDKNLA-----KVSSLLNRMANY----QGAKEHEEAENITNL TTEG 177  
 YE E +E FDKNLA KVSSLLNRMANY QGAKEHEEAENIT EG  
 Sbjct: 128 YE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRMANYTNLTQGAKEHEEAENIT----EG 181

Query: 178 KKKPTKTPQMG-----LQNI FGVT FMGVYILFLRLLPCTWVVG TAGVLQAF AIVLI 228  
 KKKPTKTPQMG LQNI FGVT ILFLRL TWVVG TAGVLQAF AIVLI  
 Sbjct: 182 KKKPTKTPQMGT FMGVYPPCLQNI FGVT-----ILFLRL---TWVVG TAGVLQAF AIVLI 232

Query: 229 CCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLGTTFEIFLVYEFGGAVGLCF-- 286  
 CCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP EFGGAVGLCF  
 Sbjct: 233 CCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP-----EFGGAVGLCFYL 280

Query: 287 ----AAAMYILGAI-----IVPRAAIFHSDDALKESAAMLNNMRVYGTAFLVLMVLVVF 336  
 AAAMYILGAI IVPRAAIFHSDDALKESAAMLNNMRVYGTAFLVLMVLVVF  
 Sbjct: 281 GTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDALKESAAMLNNMRVYGTAFLVLMVLVVF 340

Query: 337 IGVRYVNKFASXFLACVIVSILAIYAGAIKSSFAPPHPVCMLGNRTLSS--IDVCSKTK 394  
 IGVRYVNKFAS FLACVIVSILAIYAGAIKSSFAPPHPVCMLGNRTLSS IDVCSKTK  
 Sbjct: 341 IGVRYVNKFASLFLACVIVSILAIYAGAIKSSFAPPHPVCMLGNRTLSSRHIDVCSKTK 400

Query: 395 EINNMTTRHVPSK-----NATCDECNSSYFVHNNVQFFTSIQGIPGLASGIITE 442  
 EINNMT VPSK NATCDE YFVHNNV TSIQGIPGLASGIITE  
 Sbjct: 401 EINNMT--VPSKLWGGFCNSSQFFNATCDE----YFVHNNV---TSIQGIPGLASGIITE 451

Query: 443 NLWSNYLPKGEIIEK----SSDVLGSLNHEYVLVDPSAKITTSFTLLVGIFFPSTVGIMA 498  
 NLWSNYLPKGEIIEK SSDVLGSLNHEYVLVD ITTSFTLLVGIFFPSTVGIMA  
 Sbjct: 452 NLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLVD---ITTSFTLLVGIFFPSTVGIMA 507

Query: 499 GSNRSGDLKDAQKSIPIGTILAILTTS LWGFFVYLSNVVLFGACIEGVVLRDKFGVGTL 558  
 GSNRSGDLKDAQKSIPIGTILAILTTS FVYLSNVVLFGACIEGVVLRDKFG  
 Sbjct: 508 GSNRSGDLKDAQKSIPIGTILAILTTS-----FVYLSNVVLFGACIEGVVLRDKFG---- 558

Query: 559 SWPSFFSTCGAGDAVKGNLV-----PWVIVIGS-----LQSLDNIITGAPPFLR 602  
 DAVKGNLV PWVIVIGS LQSL TGAP  
 Sbjct: 559 -----DAVKGNLVVGTLSWPSPWVIVIGSFFSTCGAGLQSL----TGAP---- 598

Query: 603 WALLRLLQAIK-----VFGHSKANGEPT-----GILIASLDFFLMCYLF 642  
 RLLQAIK VFGHSKANGEPT GILIASLD  
 Sbjct: 599 ----RLLQAIKDNIIIPFLRVFGHSKANGEPTWALLLTAAIAELGILIASLD----- 646

Query: 643 TLLRLTAALVAPIAELILSM-----CALQ-----RYYHWALSFMGM 678  
 LVAPI LSM CALQ RYYHWALSFMGM  
 Sbjct: 647 -----LVAPI----LSMFFLMCYLFVNLCALQTLLRTPNWRPRFRYYHWALSFMGM 694

Query: 679 TPNWVNLARPRPRFSICLALMFI-----VAMVIAGMIGAESSWYAIYKXIEYQSLS 731  
 SICLALMFI VAMVIAGM IYK IEYQ  
 Sbjct: 695 -----SICLALMFISSWYAIAMVIAGM-----IYKIEYQG-- 727

Query: 732 PHTDEDEWGDGIRGL---AARFALLRLEEGP---KNWRPQLLVLLKL-----HPRLLT 778  
 E EWGDGIRGL AARFALLRLEEGP KNWRPQLLVLLKL HPRLLT  
 Sbjct: 728 ---AEKEWGDGIRGLSLSAARFALLRLEEGPPHTKNWRPQLLVLLKLDEDLHVKHPRLLT 784

Query: 779 FASQLKGNFLHVKGXGXTIVGSIIVG-----EALAAEQTIKHVVACGLLENYLMEAE 831  
 FASQLK AGKG TIVGSIIVG EALAAEQTIKH LMEAE  
 Sbjct: 785 FASQLK-----AGKGLTIVGSIIVGNFLENYGEALAAEQTIKH-----LMEAE 827

Query: 832 KVKGFCQL---AKLREGISH-----GGMKHNTVVLIQSMGWPNQWRQSERVTTDARAW 881  
 KVKGFCQL AKLREGISH GGMKHNTVV MGWPNGWRQSE DARAW  
 Sbjct: 828 KVKGFCQLVVAAKLREGISHLIQSCGLGGMKHNTVV---MGWPNGWRQSE----DARAW 879

Query: 882 KTFIGTVKNINIDLPAHAHLALLVA---SFFPSNVEQFSEG---VWVIVHDGGMMLLL-- 933  
 KTFIGTV+ + AHAHLALLVA SFFPSNVEQFSEG VWVIVHDGGMMLLL  
 Sbjct: 880 KTFIGTVR-VTT----AHAHLALLVAKNISFFPSNVEQFSEGNIDVWVIVHDGGMMLLLPF 934

Query: 934 -LKQHKVWRK-----TVAQLEDNSISCSIQMK---ATFLYHLRIEAEVRIFKDLEVVRT 983  
 LKQHKVWRK TVAQLEDNSI QMK ATFLYHLRIEAEV EVV  
 Sbjct: 935 LLKQHKVWRKCSIRIFTVAQLEDNSI----QMKKDLATFLYHLRIEAEV-----EVV-- 982

Query: 984 LEMHSDISAYTYERHMLSKMMEQRSQML-----TERDRIAQLVKDRNSMLRLTSIG 1036  
 EMHSDISAYTYER + MMEQRSQML TERDR AQLVKDRNSMLRLTSIG  
 Sbjet: 983 -EMHSDISAYTYERTL----MMEQRSQMLRHMRLSKTERDREAQLVKDRNSMLRLTSIG 1037

Query: 1037 SDEDEETETTTWKDKYMAQDLLHTAVYQEKVHM-----SRGQKAKSMEGF----NM 1083  
 SDEDEETET YQEKVHM SRGQKAKSMEGF NM  
 Sbjet: 1038 SDEDEETET-----YQEKVHMTWKDKYMASRGQKAKSMEGFQDLLNM 1080

Query: 1084 RPDQSNVRRM----KLNEVIVNKSHEAKLVLLNMPGPPRNPEGDENYMEFLEVLTGELER 1139  
 RPDQSNVRRM KLNEVIVNKSHEAKLVLLNMPGPPRNPEGDENYMEFLEVLTGELER  
 Sbjet: 1081 RPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNMPGPPRNPEGDENYMEFLEVLTGELER 1140

Query: 1140 VLLVRGGGSEVITIYS 1155  
 VLLVRGGGSEVITIYS  
 Sbjet: 1141 VLLVRGGGSEVITIYS 1156

☐ >gi|33329256|gb|AAQ10028.1| ☒ K-C1 cotransporter KCC3a-S2 isoform [Homo sapiens]  
☒ gi|33329254|gb|AAQ10027.1| ☒ K-C1 cotransporter KCC3a-S1 isoform [Homo sapiens]  
 Length = 1091

Score = 2350 bits (5535), Expect = 0.0  
 Identities = 868/1303 (66%), Positives = 872/1303 (66%), Gaps = 419/1303 (32%)

Query: 60 MSEMSPDPSDLSONSGHKAEGDEYMDTRPGATTSLATVAL-----RTSHPQDVIED--- 111  
 MSEMSPDPSDLSONSGHKAEGDEYMDTRPGATTSLATVAL RTSHPQDVIED  
 Sbjet: 1 MSEMSPDPSDLSONSGHKAEGDEYMDTRPGATTSLATVALDPPSDRTSHPQDVIEDLSQ 35

Query: 112 --ITGEHSQLLDD----QRNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNR 154  
 ITGEHSQLLDD RNAYLNNSNYE E +E FDKNLA KVSSLLNR  
 Sbjet: 36 NSITGEHSQLLDDGHKKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNR 93

Query: 155 MANY----QGAKEHEEAENITNLTTGKKKPTKTPQMG-----LQNIFGVTFMGVY 201  
 MANY QGAKEHEEAENIT EGKKKPTKTPQMG LQNIFGV  
 Sbjet: 94 MANYTNLTQGAKEHEEAENIT----EGKKKPTKTPQMGTFMGVYLPCLQNIFGV----- 143

Query: 202 ILFLRLLPCTWVVGTAFLVLAFAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRA 261  
 ILFLRL TWVVGTAFLVLAFAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRA  
 Sbjet: 144 ILFLRL---TWVVGTAFLVLAFAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRA 200

Query: 262 LGPYLGTTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDA 309  
 LGP EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDA  
 Sbjet: 201 LGP-----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDA 248

Query: 310 LKESAAMLNNMRVYGTAFLVLMVLVVFIVGVYVKNKFASXFLACVIVSILAIYAGAIKSSF 369  
 LKESAAMLNNMRVYGTAFLVLMVLVVFIVGVYVKNKFAS FLACVIVSILAIYAGAIKSSF  
 Sbjet: 249 LKESAAMLNNMRVYGTAFLVLMVLVVFIVGVYVKNKFASLFLACVIVSILAIYAGAIKSSF 308

Query: 370 APPHFPVCMLGNRTLSS--IDVCSKTKEINNMTTRHVPSK-----NATCDECNS 415  
 APPHFPVCMLGNRTLSS IDVCSKTKEINNMT VPSK NATCDE  
 Sbjet: 309 APPHFPVCMLGNRTLSSRHIDVCSKTKEINNMT--VPSKLWGFFCNSSQFFNATCDE--- 363

Query: 416 SYFVHNNVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK----SSDVLGSLNHEYVL 471  
 YFVHNNV TSIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLGSLNHEYVL  
 Sbjet: 364 -YFVHNNV---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVL 419

Query: 472 VDPSAKITTSFTLLVGIFFPSTGIMAGSNRSGDLKDAQKSIPIGTILAILTTSWLGFFF 531  
 VD ITTSFTLLVGIFFPSTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS F

Sbjct: 420 VD----ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS-----F 470

Query: 532 VYLSNVVLFGACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIV 583  
VYLSNVVLFGACIEGVVLRDKFG DAVKGNLV PWVIV

Sbjct: 471 VYLSNVVLFGACIEGVVLRDKFG-----DAVKGNLVVGTLSWPSFWVIV 514

Query: 584 IGS-----LQSLDNIITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT- 626  
IGS LQSL TGAP RLLQAIK VFGHSKANGEPT

Sbjct: 515 IGSFFSTCGAGLQSL----TGAP-----RLLQAIKDNIIIPFLRVFGHSKANGEPTW 562

Query: 627 -----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----C 663  
GILIASLD LVAPI LSM C

Sbjct: 563 ALLLTAAIAELGILIASLD-----LVAPI----LSMFFLMCYLFVNLC 602

Query: 664 ALQ-----RYYHWALSFMGMTPNWVNLRPRPRFSICLALMFI-----VAM 704  
ALQ RYYHWALSFMGM SICLALMFI VAM

Sbjct: 603 ALQTLRLTPNWRPRFRYYHWALSFMGM-----SICLALMFISWYYAIVAM 648

Query: 705 VIAGMIGAEKSSWYYAIYKXIEYQSLSPHTDEDEWGDGIRGL---AARFALLRLEEGP-- 759  
VIAGM IYK IEYQ E EWGDGIRGL AARFALLRLEEGP

Sbjct: 649 VIAGM-----IYKIEYQG-----AEKEWGDGIRGLSLSAARFALLRLEEGPPH 692

Query: 760 -KNWRPQLLVLLKL-----HPRLLTFASQLKGNFLHVKGXGTIVGTVIVG----- 805  
KNWRPQLLVLLKL HPRLLTFASQLK AGKG TIVGTVIVG

Sbjct: 693 TKNWRPQLLVLLKLDEDLHVKHPRLLTFASQLK-----AGKGLTIVGTVIVGNFLENY 745

Query: 806 -EALAAEQTIKHVVACGLLENYLMEAEKVKGFQCL---AKLREGISH-----GGMKHN 854  
EALAAEQTIKH LMEAEKVKGFQCL AKLREGISH GGMKHN

Sbjct: 746 GEALAAEQTIKH-----LMEAEKVKGFQCLVVAAKLREGISHLIQSCGLGGMKHN 795

Query: 855 TVVLIQSMGWPNGWRQSERVTTDARAWKTFIGTVKNINIDLPPAAHLALLVA---SFFPS 911  
TVV MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPS

Sbjct: 796 TVV----MGWPNGWRQSE----DARAWKTFIGTVR-VTT----AAHLALLVAKNISFFPS 842

Query: 912 NVEQFSEG---VWWIVHDGGMMLLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK 959  
NVEQFSEG VWWIVHDGGMMLLL LKQHKVWRK TVAQLEDNSI QMK

Sbjct: 843 NVEQFSEGNIDVWWIVHDGGMMLLLPFLKQHKVWRKCSIRIFTVAQLEDNSI----QMK 898

Query: 960 ---ATFLYHLRIEAEVRIFKDLVVRTLEMHDSDISAYTYERHMRSLKMMEQRSQML--- 1013  
ATFLYHLRIEAEV EVV EMHDSDISAYTYER + MMEQRSQML

Sbjct: 899 KDLATFLYHLRIEAEV-----EVV---EMHDSDISAYTYERTL----MMEQRSQMLRHM 945

Query: 1014 ----TERDRIAQLVKDRNSMLRLTSIGSDEDEETETTWTCKDYMAQDLLHTAVYQEKVHM 1069  
TERDR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM

Sbjct: 946 RLSKTERDREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHM 988

Query: 1070 -----SRGQKAKSMEGF----NMRPDQSNVRRM----KLNEVIVNKSHEAKLVLLN 1112  
SRGQKAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLN

Sbjct: 989 TWTCKDYMASRGQKAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLN 1048

Query: 1113 MPGPPRNPEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS 1155  
MPGPPRNPEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS

Sbjct: 1049 MPGPPRNPEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS 1091

☐ >gi|38565928|qb|AAH62099.1| Unknown (protein for MGC:69652) [Mus musculus]  
Length = 1106

Score = 2345 bits (5523), Expect = 0.0

Identities = 868/1326 (65%), Positives = 884/1326 (66%), Gaps = 422/1326 (31%)

Query: 1 MHPPETTTKMASVRFMVPTPKIDDIPGLSDTSPDXSSRSSSRVRFSSRESVPETSRSEPM 60  
MHPPE TTKM+SVRFMVPTPKIDDIPGLSDTSPD SSRSSSRVRFSSRESVPETSRSEPM  
Sbjct: 1 MHPPEATTKMSSVRFMVPTPKIDDIPGLSDTSPDLSSRSSSRVRFSSRESVPETSRSEPM 60

Query: 61 SEMSDPPSDLSQNSGHKKAEGDEYMDTRPGATTSLATVAL-----RTSHPDQDVIEDITGE 115  
SE+S GATTSLATVAL RTS+PQDV ED  
Sbjct: 61 SELS-----GATTSLATVALDPSSDRTSNPQDVTED---- 91

Query: 116 HSQLLDDQ---RNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRMANY--- 158  
D RNAYLNNSNYE E +E FDKNLA KVSSLLNRMANY  
Sbjct: 92 -----DGHKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRMANYTNL 144

Query: 159 -QGAKEHEEAENITNLTTEGKKKPTKTPQMG-----LQNIFGVTFMGVYILFLRL 208  
QGAKEHEEAENIT EGKKKPTK+PQMG LQNIFGV ILFLRL  
Sbjct: 145 TQGAKEHEEAENIT----EGKKKPTKSPQMGTFMGVYLPCLQNIFGV-----ILFLRL- 193

Query: 209 PCTWVVGTTAGVLQAFVILICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLGT 268  
TWVVGTTAG+LQAFVILICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP  
Sbjct: 194 --TWVVGTTAGILQAFVILICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP---- 247

Query: 269 TFEIFLVYFEGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDALKESAAM 316  
FEGGAVGLCF AAAMYILGAI IVPRAAIF SDDALKESAAM  
Sbjct: 248 -----FEGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFRSDDALKESAAM 299

Query: 317 LNNMRVYGTAFVLMLVLFVFIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFPAPHPFPV 376  
LNNMRVYGTAFVLMLVLFVFIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFPAPHPFPV  
Sbjct: 300 LNNMRVYGTAFVLMLVLFVFIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFPAPHPFPV 359

Query: 377 CMLGNRTLSS--IDVCSKTKEINNMTRHVPSK-----NATCDECNSSYFVHNN 422  
CMLGNRTLSS +D+CSKTKE++NMT VPSK NATCDE YFVHNN  
Sbjct: 360 CMLGNRTLSSRHLDCSKTKEVDNMT--VPSKLWGFFCNSSQFFNATCDE----YFVHNN 413

Query: 423 VQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK----SSDVLGSLNHEYVLVDPSAKI 478  
V SIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLG+LNHEYVL D I  
Sbjct: 414 V---ISIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLAD----I 466

Query: 479 TTSFTLLVGIFFPSTGTGIMAGSNRSGDLKDAQKSIPIGTILAILTTSLSWGFFVYLSNVV 538  
TTSFTLLVGIFFPSTGTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS FVYLSNVV  
Sbjct: 467 TTSFTLLVGIFFPSTGTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS-----FVYLSNVV 521

Query: 539 LFGACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIVIGS---- 586  
LFGACIEGVVLRDKFG DAVKGNLV PWVIVIGS  
Sbjct: 522 LFGACIEGVVLRDKFG-----DAVKGNLVVGTLSWPSFPWVIVIGSFFST 565

Query: 587 ----LQSLDNIITGAPPFLRWALLRLQAIK-----VFGHSKANGEPT----- 626  
LQSL TGAP RLLQAIK VFGHSKANGEPT  
Sbjct: 566 CGAGLQSL----TGAP-----RLLQAIKDNIIIPFLRVFGHSKANGEPTWALLLTAA 613

Query: 627 ----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----CALQ---- 666  
GILIASLD LVAPI LSM CALQ  
Sbjct: 614 IAEKGILIASLD-----LVAPI---LSMFFLMCYLNVNLCALQTLLR 653

Query: 667 -----RYYHWALSFMGMTPNWVNLRPRPRFSICLALMFI-----VAMVIAGMIG 711  
RYYHWALSFMGMT SICLALMFI VAMVIAGM  
Sbjct: 654 TPNWRPRFRYYHWALSFMGMT-----SICLALMFISSWYYAIVAMVIAGM-- 697

Query: 712 AEKSSWYYAIYKXIEYQSLSPHTDEDEWGDGIRGL---AARFALLRLEEGP---KNWRPQ 765  
IYK IEYQ E EWGDGIRGL AARFALLRLEEGP KNWRPQ